



## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPPCRNGGSCVQPGRRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQW  
EGHSLSADGTLCPVKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

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# FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
 GTCAGCCCCACGGCGGGGACTATGGTGAAATTCGCGGCGCTCAGCCTACTGGCCCTGTATC  
 CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA  
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
 ACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGACTTCAAAATGTGGGCTGGTGT  
 GTGAACAGCAAGAGAGACAGGACCAAAGCCGCTCTGTGTATGGTGGTGCGAGGGCCATCGC  
 TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACATGC  
 ACCATGTGGACGAGTCCGTTGGGGAGCAAGACGAGAAGGCCCTTCTGTACTCTCGCGCCTTT  
 CCTTTCATGGACGAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT  
 CCTGGTGGGATGTGCCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC  
 TTCACAGTCACTTGGAAATGCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTGTACATGGGC  
 GCACTTGTGCGCTGCACCACCTGTGCCCTGGGCTACTACAAGAACATTACGACATCATCCC  
 TGACAGAAGTGGCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
 GGCCCTTTGGCTCTAATTTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
 TCCCGGGGATCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGGATTTTGAGAGCCACATA  
 CCCTTGTGGGTCACTGCCATACCGGCTGGTTGACGGAAATCCGCTGCTGTGTATCTGTCTTTCG  
 ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC  
 AAGAAGTTCACTTTCGCTGCTGATGGCTCTGTCACTCAGCTCTGTTTTCGTGATGTTTTGGAC  
 ACCCAACGTGTCTGAGAAAACTTTGATAGACATCATCGGAGTGGACTTTGGCCTTTGCAGAAC  
 TCTGTGTGTTTCTTTGCGGATCTTCTCCTTCTCCAGTTCCAGTCACAGTAGGGCGCAT  
 CTCACCGGTGGCTGATGACACTGAAGAAAACTTCTGTCCTGTGCCCGCAGCTCTGTGCTGGG  
 GATCATCGTCCCTCATCGCCAGCCTCGTGGTCTCCTACCTACCTGGGGGTGCACGGTGCAGCC  
 TGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAAATCCACCATGGTCGCCATCGCTGGC  
 TGCTATGTCATCCGGAAGCAGAAAAAGAAATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
 CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
 AGAATGAATAAGGACCGGGACGCCATGGGCACATGCAGGGACGGTCAGTCAGGATGACACTTC  
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTTGTTTGGTAAT  
 GAAAGAGGCCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATATCGGGTATGCTCACACT  
 GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAACGAAACAACCTGAC  
 TTCATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCCTCAGGTTGACGTTGTGTCC  
 TCCTCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
 CACCTTGCACAGGGCCACAGACTCTCCTGTCCCTTTCATCGCTCTTAAGAATCAACAGG  
 TTAAACTCGGCTTCTTTGATTGCTTCCAGTCACATGGCCGTACAAGAGATGGAGGCC  
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACATGCGAG  
 GAGGCGGGTGGCAGCTGCAGCCGGAGTCCCGTTACACTGAGGAACGGAGACCTGTGAC  
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCGGG  
 GGCAGCAAATGACATGGTTGAATGATAGCATTCTACTCTGCGTTCTCCTGATCTGAGCAA  
 GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCAAAAA  
 GCGCATCTCCAGATTCCAGACCTGCGCATGACTTTTCTGAAGGCTGCTTTTCCCTCGC  
 CTTTCTGAAGGTTCGCAATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCAATTTAGTTT  
 TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC  
 TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
 TTGAGAACTACTACGGTATCTCCCTCCACACCATACGATAAAGCAAGACATTTTATAACG  
 ATACCAGAGTCACATATGTGGTCTCCCTGAAATAACGCATTGGAATCATGCAATGACGTA  
 TATTTTCTAAGTTTGTGAAGACAGGTTTTTCTCTTAAAAAAATATAGACAGGTTCACT  
 AAATTTAGTTAGTCAGAATTCTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA  
 TAAATATATGCTGATATGTTATGTAAATTTATTTAGGCTATAATACATTTCTTATTTTCG  
 ATTTTCAATAAAATGCTCTCAATACAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSEDFKNVGLVFNNSKRDRTKAVLCMVVAGIAAVFHTLIAYSDLGYIINKLHHVDES  
GSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSPFWWPLALIL  
ATQRISRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNPNPSN  
KLVSTSNVTAAHIKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR  
IFSFFPVFPVTVRAHLTGWLMTLKKTFVLAPSSVLRRIIVLIASLVLPYLGvHGATLGvGSLl  
AGFVGESTMVAIAACYVYRKQKKKMenESATEGEDSAMTDMPPTeeVTDIVemREENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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## **FIGURE 5**

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTGGAC  
ACCCAACGTGTCTGNGAAAACTTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGGCAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTCAGAAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCCTTTGCAGAANTTTGNGNTGTTCCTTTGCGGATTTTCT  
CCTTTTTCCCAGTTCAGTCAACAGNGAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATGTCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCAGCCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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## FIGURE 8

GCCCCGCGCCCGCGCGCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCTCTGCCTCTGCGGCTCTGCCCTGCATCCTGTGCGAG  
CTGCTGCCCGCGCAGCCGCAATCCACCGTGAGCGCCTCATCTTCAGTCTCTCTCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGAGAGTCACTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCGGGATCCCCACCGTCTGCGAGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT  
TCTTTTTCACCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGGGGCTCCTTCTCTTCA  
TCCTCATCCAGCTGGTGTCTGCTCATCGACTTTCGCGACTCCTGGAACAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCATTCCTGCTGCTGTAACGAGCGCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGTCTGATCGCGCGCTGGCGCTGATGTTTCATGTACTACACTGAGCCGAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCCTCGGTCT  
CACCCCTTACACCATGTTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCGAGCATTTGTGGGCTCATCATCTTCTCTGTCACCCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACAAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGSCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACTACAGCTACTCCTTCTTCCACTTCTGCTGGTGCT  
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCAGTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCTTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACT  
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG  
CCCCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGTCGAGGAGCATCAGGCTCCTGCA  
GAGCCCTACCCCCGACACACCGGTGGAGCTGCCTCTTCTTCCCCCTCTCCCTGT  
TGCCCTACTCAGCATCTCGGATGAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACCTCCACCAAGTGGGGCATCCGGCACTGAAGCCCTGGTGT  
CCTGGTCACTCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

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## **FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SPLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWYFVGVSFLFILIQLVLLIDFAHSW  
NQRWLKAECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTF  
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVA  
ACEGRAFDNEQDGVTSYSFFHFCVLVSLHVMMLTNWYKPGETRKMISTWTAVVVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACTGGGTCT  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGGGCACGTCCGCGAGGACTTGA  
AGTCTCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCATTATTTCCCGAGTCTTTTGCTGCCGAAGCTG  
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCTGAGGAGCGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTCTTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA  
GCTGTACCGGAAGTCTTTTATAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAAGAAAGAAAACAGAAGGATCGAAAGGCACCTCCATGAGCTAAAACCTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAAACAAGACAAGGACTGAAAGTGTCTTGAACCTGAAACCTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTCTT  
TTTAACTAAGAATGGGGCTGTGTGACTCTCACTTTACTTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAACTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
CGAGTAAATAAAACATTTTCGAAAAGATTAAAGTTGAATTTTACAGTTT

# DESIGN

### Important Features:

amino acids 1-24

amino acids 76-96 and 171-195

amino acids 153-156

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGCTTCATG  
GCTGGCGCCGAACC

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050910

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## FIGURE 14

GAGCCGCCGCCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGGCCCCACCCACGTCT  
GCGTTGCTGCCCCGCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT  
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTTCGGGG  
GCTTCGCGTGTTCCAAGAACTGCCGTGCGCCCTCAACCTGCTTTACACCTTGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCAGTCTCCGAGTGGT  
CGGCGTGGTCATTGCAGTGGGCATCTTCTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT  
GTTCAGTTTTCTGTATCTTGCCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGITTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCGCGCAATCCTAGTGCATTCTTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCGTATATGATCTGTTCACTTTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACACTATCTGAAAAGTACCTTATTGATAGTGAATATATATTTTTACT  
CTATGTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTTCATTGTGCGGCACTGTCCACTGTGGCCTT  
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGTTACCACTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCTAC  
TGGAAAAAGAGTGGAAATTTATTAATAATCAGAAAGTATGAGATCCTGTATGTTAAGGGAAA  
TCCAAATCCCAATTTTTTTTGGTCTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATGTGGTTTAAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACAGCAACTT  
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTGTGTATGCATGTTTGA  
ATTAAGGAAAGTAATGGAAG

[illegible]

```
><subunit 1 of 1, 204 aa, 1 stop
```

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFLGISSLRVVGVIAGVIFLFLIALV  
GLIGAVKHQQVLLFFYMIILLLVFIVQFSVCACALNQEQQGQLLEVGNWNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFGVGGIGLFFSFTEILGVWL  
TYRYRNQKDPANPSAFL

amino acids 1-34

amino acids 47-63, 72-95 and 162-182

## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

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## **FIGURE 17**

AATCCCAAATCCCCAATTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

## FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

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## FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACCTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGCCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCTCTGGGATCCAGAAAACGACATCTGTTGTGGCTAT  
CACAGTCCAAGAAGTGTTCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTTGAGAGGTGAGCTGCCCCG  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTGTTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAAGGTGCTTCCAGCTCT  
GCTGCACCTCCCAATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTGTCTCTGA  
GGAGGCCCCCTGGGCTCTGCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCCTTCTTCAAACACATG  
CAGGATGTGAGAGTCTCTCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCTGGGACCAAAAGGCTACTGCTGAATAGAAGTAAACAGTTTCATCCATGATCTCACT  
TAACCAACCCCAATAAATCTGATTCTTTATTTTCTCTCCTGTCTGACATATGCATAAGTA  
CTTTTACAAGTTGTCCAGTGTTTTGTGTAGAATAATGTAGTTAGGTGAGTGTAAATAAATT  
ATATAAAGTGAGAAATTAGAGTTTAGCTATAATTGTGTATTCTCTTAAACAAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAAATGTTGTGATTTAAAGGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCACTGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAACATCCTATAATGCACAG  
GGCAGTACCCCAACAACGAAAATAATCTGGCCCAAATGTCAAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCTAGGTGTGGGCTCTGGAATGGGACTTTTGCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAGTGGGCTTTGGGAAGTGATTAGATCAGGAGTGAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCCAAACACCG  
ACTCTGTCTGTGCTTGTATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG  
TTGTTTGTAGCCTAA

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## FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSGALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

## FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAGAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCTTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCA CCTATG  
ACCCCTGCAAGGCTACACCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTCGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACAGGAACCCATC  
AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCCTGACATGGATGGCTACCT  
TGGAGAGACCAAGTGTGGGCCAGGAAAGAGCCTGCTGCTTTGCCATCATCTCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCAATTTTGAACCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAATGTGGAGGAAGGGGGGTGTGGCCACAGACCC  
AATCCTAAGGCCGAGGCTTCAAGGCTCAGGACATAGCTGCCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAAATTGAGGCAGAAAGGTTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGTTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACCTCCAGAATCTGGGCAACAACCTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCCGAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCTTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCCAGGGCCAGACAGCTTTAATTGAATTTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

0978193.101501

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVRGS  
DPVTIFLRDSSGDHIQQAKYQGRLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLQCQARGSPPISYIWKQQTNQOE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

## FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCA CGGGGCGCGGGGCGGGCTCCCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGGCGCGCGCCAGCTCGCCCGAGGTCCGTCGGGA  
GGCGCCCGGGCGCCCCGGAGCCAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGGATGTCTCCCTCCTCTCTCTCTCTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGAAAAGGTCACTTTGCCCTGCCACCATCACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCTATGCTACAATAACTTGACTGAGGAACAGAAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCTTGCAAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGATT  
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT  
GACTACAACCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
CCAGTGCACAGCAGGCAACGAAAGTGGGAAGGAAAGCTGTGTGGTGCAGTAACCTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCTCTTGGTTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCAGCT  
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGGTTCTTCTCCTCCTCCTCCACAGCAAAAT  
AGTGCTCTCAGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGCCAC  
CCAGGCATACAGCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG  
CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCACCAGCCAGAGCAGAGCCCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCACCGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTTCAGATGAGCATTTTCTTTATACAATACCAACAAGCAAA  
AGGATGTAAGCTGATTCTCTGTAAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAACCTTTAATGTGGGATATTTTGATCAGTGCTTTGATTCACAATT  
TTCAAGAGGAAATGGGATGCTGTTGTAAATTTTCTATGCAATTTCTGCAAACTTATTGGATT  
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACTGCTACACCATGTAC  
TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTACATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCTCAAAT  
CAGATGCCCTCAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCATT  
TATCAACGTCTTAGAAAGAAATCTCTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTAAGTCTCTTCTTCTGAGAAATGTGAACCAAGAAATTCAGAGCTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCTGGGTGACAGAGCGGGACTCCGCTC

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRRHVNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251





## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSFSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEIKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVKKGTETEDVRCKQCARGTFSVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYALQHWTIIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSQDKNGKGFVDESEPLL  
RCDSTSSGSSALSRRNGSFITKEKDDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLEFIIQVKSQEASQTLSDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

# FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA  
CTCGGGAATTTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTGAAATAGTCAC  
CATGGGGGAAAAATGATCCGCTGCTGTTGAAGCCCCCTCTCATTTCCGATCGCTTTTGGCC  
TTGATGATTGAAAATAAGTCTGTGTCACAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGGAAGTACAGATGTCGCTCATCTCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGTGGGTGCTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATTGTGCTCCGATGACTGGAAGGGTCACTACGCAATGTTGCCCTGTGCCAAC  
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGGCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCCTCTGGCCACGTTGGTTACCTTGCAGTGCACAGCCT  
GTGGTCATAGAAGGGGTACAGCTCAGGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACTGTGCGGGGGCTCTGTCATCAC  
GCCCTGTGGATCATCACTGTGACACATGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
ATTGCTTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGGCACTCAGTTCATGAAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAGA  
ACTTCCCCGATGGAAGAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCGTCTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACAGCCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGGTACAC  
CCGTGTCACTCCTTCTGGATCGATCCACGAGCAGATGGAGAGAGACCTAAAAACC**TGAA**  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTCTGAGGTGATGAAGACAGCCCGATCTCCCT  
GGACTCCCCGTGTAGGAACCTGCACACGAGCAGACACCTTGGAGCTCTGAGTTCGGGACCA  
GTAGCAGGGCCGAAAGAGGCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT  
GTTTTTTGTTTTTTTGGAGTGGAGTCTCGCTCTGTTGCCACAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAGAGCATTTCTCTTGCTCAGCTTCCCA  
GTAGCTGGGACCACAGGTGCCCCGCCACCACACCACTAATTTTTGATATTTTGTAGTAGAGAC  
AGGGTTTCAACATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCGTGCTT  
CAGCCTCCCAAGTGTCTGGGATTACAGGCATGGGCCACACGCTAGCCTCAGCTCCTTTT  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGCGGCCCTTTCCTACTGGTCCAT  
CTGGTTTTCTCCAGGCTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAGC  
TGCAAGGCCAACACGCCACTCAGAAAAAGACGACACAGCCGAGTGCAGAACTGCAGTCACT  
ACTGCAGTTTTTCATCTTAGGGACAGAACCAAAACCCACCTTTCTACTTCAAGACTTAT  
TTTCAATGTGGGGAGTTAATCTAGGAATGACTCGTTTAAAGCCATTTTTCATGATTTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCTTCCCT  
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

09978193.101504

01234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991300

><subunit 1 of 1, 453 aa, 1 stop

MGENDPPAVEAPFSPFSLFGLDDLKISPVAPDADAVAAQILSLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVILQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSLBGGQFREEFVSIIDHLLPDDKVLTALHH  
SVYVREGCASGHVVTLLQCTACGHRRGYSSRIVGNGMSLLSQWPWQASLQFGYHLCCGGSVIT  
PLWIIITAAHCYVDLYLPKSWTIQVGLVSLLDNAPSHLVEKIVYHSKYKPKRLGNDIAlMKL  
AGPLTFNEMIQPVCLPNSENFDPGKVCWTSGWGATEDGGDASVPLNHAAVFLISNICKNHR  
DVYGGIISPSMLCAGYLTEGGVSDCQGDGGGLVLCQERRLKLVLGATSFSGIGCAEVNKPQVYT  
RVTSFLDWIHEQMERDLKT

amino acids 1-20

amino acids 240-284

# FIGURE 29

CCCACGCGTCCGTCTTAGTCCCGGGCCAACTCGGACAGTTTGCTCAITTTATTGCAACGGTCAAGGCTGGCTTGT  
 GCCAGAAACGGCGCGCGCGCGCAGCACAGCACACACGCGGGGAAACITTTTAAAAATGAAAGGCTAGAAGA  
 GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGSGCTCCGGAGCTGACTCGCCGAGCGAGGAAATTCCTCCGGTCGCGA  
 CGCCCGCGCGCGCTCGCGCGCCCGCGTGGGATGGTCTGAGCGCTCGCCCGCGCGGCGCGAGCTGCTGCAGATGAAG  
 GCGCGCGACGATGCGAGCGCGCGCGCTGCCCCGTGTCGCCCGCGCGCGCTCTGCTCGCCCTGGCGGCTGCTCT  
 GCTCGCGCCCTGCGAGGCGCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAGTTGTTCAGTGCCTCTGT  
 TCGGATGGGAGCTCTGGATCCCAAGTGAAGAGCTTCGACTCCAAGATCATCCAGAGTGTGTAATATTGACT  
 ACAACGGGAAAGCAAAAGACTGATCATAAATCTGGAAGAAATGAAGGTCTCAITGGCCAGCAGTTTACGCGAAAC  
 CCATATCTGCAAGAGCGGTACTGATGTCTCCCTCGCTCGAAATACACGGGTCACTGTGTACACCATGGAGATGT  
 ACGGGATATTCTGATTTCAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGCGGACTTATTGTGTTTGAAGATGA  
 AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCAGCGGAAGAAGCTGAAAAGCGT  
 CCGGGATCATGTGGATCACATCAACACACCAAACTCGCTGCAAGAAGTGTGTTCCACCAACCTCTCAGAC  
 ATGGGCAAGAGGCATAAAAGAGAGACCTTCAAGGCAACTAAGTATGTGGAGCTGGTATCTGGCGAGACCAACG  
 AGAGTTTCAGAGGCAAGGAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGTCTAATCACTGTGACAA  
 GTTTTACAGACCACTGAACATTCCGATCGTGTGTTGGTAGGCGTGGAAAGTGTGGAATGACATGGCAAAATGCTCTGT  
 AAGTCAGGACCAATTCACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA  
 TGACAAATGCGCAGCTTGTGATGTTGGGTTTATTTCCAAAGGACCAACATCGGCTGGCGCCCAATCATGAGCATGTG  
 CACGCGCAGACCACTGGGGGAATTTGTCATGGACCAATCAGACAAATCCCTTGGTGCAGCGGTGACCTTGGCACA  
 TGAGCTGGGCGCAAAATTCGGGATGAATCATGACACACTGGACAGGGGTGTAGCTGTCAAATGGCGGTTGAGAA  
 AGGAGGCTGCATCATGAACGCTTCCACCGGTAACCAATTTCCATGGTGTTCAGCAGTTTCAGCAGGAAGGACTT  
 GGAGACCAAGCTGTGAGAAAGGAATGGGGGTGTGCTGTGTTAAGCTGCGGAAAGTCAAGGAGTCTTTCCGGGGCCA  
 GAAGTGTGGGAACAGATTTGTGGAGAAGGAGAGAGTGTGACTGTGGGAGCCAGAGGAATGTATGAATCGCTG  
 CTGCAATGCGCACCTGTACCTGTAAGCCGAGCGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
 GAAGCTGTCAGGAACAAGGTGTCAGGAGCTCCAGCAACTCTGTGACCTCCAGAGTGTGCAAGAGCTGCCAGCT  
 TCACTGCCCAAGCAATGTGACTGTCACGATGGGCACTCATGTGAGATGCGAGGCTGACTGCTACCAATGGCAT  
 CTGCAGACTCTCAGGAGCAGCTGTGTCACGCTCTGGGACCAAGGTGCTAAAGCTGCCCTGGGATCTGCTTTGA  
 GAGATCAATCTGCAGGTGATCTTATGCAACTGTGGCAAAGTCTCGAAGAGTCTCTTTGCCAAATGCGAGAT  
 GAGAGATGCTAAATGTGCAAAATCAAGTGTCAAGGAGTGGCAGCCGCGAGTCAATGGTACCAATGCGCGTTTC  
 CATAGAAAACAACTCCCTTCAGCAAGGAGGCGGATTTCTGTGCGGGGACCCAGCTGACTTGGCGCATGA  
 CATGCGGACCAAGGGCTTGTGCTTGCAGGCACAAAGTGTGAGATGGAATAATCTGCTGAATCTCAATGTCA  
 AAATATTAGTGTCTTTGGGTTTCAGAGTGTGAATGCAAGTGCAGTGCACGCAAGGGGTGTGCAACACAGGAAGA  
 CTGCCATGCGAGGCCCATCGGCGACTCCCTTCTGTGCAAGTTTGGCTTTGGAGGAGCAGCAGACGCGGCC  
 CATCCGGCAGCAGAGCAAGCAGGCAAGGCTGAGAGTCCAGAGGAGCGCGCGCAGGGCAGGAGCCGTGGG  
 ATCGCAGGAGCATCGCTCTACTGCTCATGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAATG  
 CTGCTGAGAGGAGGTCAAGCGTCCCCAAGGCTCCTGTGACTGCGCAGCTTACTCTGTGGCTTTGGCCATCGTT  
 TCCATGACAAACAGACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCTTACAGGCAAGCTGTCAGAAA  
 CAGTGCAGGAAGGGCAGCGACTTCTGTTGTGAGCTTCTGCTAAACATGAGCATGCTTCAGTGTGCTCTGAG  
 AGAGTAGCAGTTTACCACTCTGGCAGGCCCGACCTGTCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCTTTTC  
 ACTGAGCTTCCACAGCAGTGGGGGAGAAGCAAGGGTGGGCCAGTGTCCCTTTCCCCAGTGACACCTCAGCCT  
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTTATGAAAAT  
 AGCAGGGTTTGTGTTTAAATTTATGAGAACCTGCCACCCATTCCATCCAAAGCAAACTGAATGGCAA  
 TGAACAACACTGGAAGAAGGTAGGAAGAGGGCGGTGAACTCTGGCTCTTTGGCTGTGGACATGCGTGAACAGC  
 AGTACTCAGGTTTGTAGGGTTTGCAGAAAGCAGGGAACCCACAGAGTCAACCAACCTTCAATTTAAACAAGTAAGAA  
 TGTTAAAGGTGAAAACAAATGTAAAGACTTAATCCATCCCGGTGCCATTACTGTCATAAAATAGAGTGCAATT  
 GAAAT

0070303.101501

[illegible]

><MW: 80177, pI: 7.08, NX(S/T): 5

amino acids 1-28

## **FIGURE 31**

TCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANNTTCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCAGTGAACCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

0978193.104504

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCAGTGCAACCACACCCGGCCACAACTTTTTAAGAAGTTAAT  
GAAACCATACCTTTTACATTTTTTAATGACAGGAAAAATGCTCACAATAATTGTTAAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAAATA  
TACCAAAATATCAATAATACTTTATCTCTGGGTAAAAACCTCTTCTCATACCTGTGTCTAACAA  
CTTTTAAACAAAAAATTTGCATCACTTTTAAAGATCAAGAAAAATTTCTGAAGGTCAATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGGAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGAGTGATGCTACTGCCATTATGATGCCCC  
TTGAATATAAGACCTTACTTGCTATCTCCCCTGACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGCCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCTACCCGTGCAGGTTTTCTCATTTGTT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCTT  
ACAGCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTGAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATAATTGACTGGCGTGGTGGTGAGTGCCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCTGTAATCCCGGCCTTTGGGAGGCCGAGGTGGGCGGATCACAGGTCAGGAGATCA  
AGACCATCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 33**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309
```

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLIILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLAL  
LHLYH

Signal peptide:

amino acids 15-27



## **FIGURE 35**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAADGGQDPHS
KHLYTADMFTTHGIQSAAHFVMMFFAPWCCHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCIAH
SDVCSAQGVVGYPTLKLKFKPGQEAVKYQGPRDFQTLNWMMLQTLNNEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCCHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGGKVDQYKGRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCCHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLFRGGKKVSEHSGGRDLDSLHFRVLSQAKDEL
```

**Signal sequence:**

amino acids 1-32

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## FIGURE 36

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTA  
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTGGGTGTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCGAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAA

## **FIGURE 37**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLQLIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNVIAIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

0976193.101503

# FIGURE 38

GGTTCTATCGATTCSAATTGCGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
 CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATCGGGCGTGT  
 GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTT  
 CGGAAGGGAGGATCAGGGATGTTTGCAGCGCGCTGGAACAGACGGTGCCGATAGAGGAAGC  
 GGGCTCCATGGCTGCCTCTGTGCTGCCCTGTCTGTTGCTACCGCTGCTGCTGCTGA  
 AGCTACACCTCTGGCCGAGTGTGCGCTGGCTTCCGGCGGACTTGGCCCTTTCGGCTGCGAGT  
 CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCCGGGTGC CGCCGACCCGGAAGG  
 TCCCGAGGGGGGTGCGAGCTTGGCTGGCCCTCGCGAACTGGCCAGCAGCGCCGCGC  
 ACACCTTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
 AGGGCTGCAACGCGCTTCTCTACGTGCGCTAGGCTGGGACTGGGACCCGACGGCGGCAGAG  
 CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGAGATGCAAGCGCCG  
 GAAGCGGCGCGGAGTTTCCGGAGGGGACGCTGCGCCAGAGGTGGAGGAGCCGCGCCCT  
 CTGTCACTGGAGCAACTGTGGCGTGTCTCTCCCCGCTGGGCCAGAGTTTCTGTGGCTGTG  
 GTTCGGGCTGGCCAAAGGCGCGCTGCGCACTGCTTTTGTGCCACCGCCCTGCGCCGGGGC  
 CCCTGCTGCACTGCTCCGAGCTCGCGCGCGCGCGCTGGTGTGCGCGCAGAGTTTCTG  
 GAGTCTCTGGAGCCGAGCTGCCCGCTTGAGAGCCATGGGCTCCACCTGTGGGCTCGAG  
 CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
 GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACAGTGCCTGTACATCTTC  
 ACCTTGGGCACCAAGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
 CCAGGGCTTCTATCAGCTGTGTGTGTCACACAGGAAGATGTGATCTACCTCGCCCTCCAC  
 TCTACCACATGTCCGTTTCCCTGTGGGCATCGTGGCTGCATGGGCATTGGGGCCACAGTG  
 GTGCTGAATCCAAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
 GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGCCCCGAGCAGAGGCAG  
 AACGTGCCCATAAAGTCCGGCTGGCAGTGGGCAGCGGCTGCGCCAGATACCTGGGAGCGT  
 TTTGTGCGGCGCTTCCGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
 GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC  
 ATATCTTCCCTTCTCTTTCGTTGATTCGCTATGATGTACCAGAGGAGAGCCAATTCCGGACCCC  
 CAGGGCGCATGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAAGCA  
 GCAGTCCCACTTCTTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG  
 ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
 GGTCTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAAATGTGGC  
 CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
 GAGTCACTGTGCCAGGGCATGAAGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
 CACGCTTTTGACCTTATGCACTCTACACCCAGCTGTCTGAGAACTTGCACCTTTATGCCG  
 GCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACACAGAGACCTTCAACAGCAGAGAAAG  
 TCTCGATGGCAAAATGAGGGCTTCGACCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC  
 CAGGCTGTAGGTGCTTCCCTCACAACCTGCGGTCACAGCGCCCTCTGTGGCAGGAAA  
 CCTTCAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGTGGGG  
 CCGTTGCAGGTGTACTGGGCTGTCAAGGATCTTTTCTATACAGAACTGCGGTCACTATTTT  
 GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGTACCTAAAAAAGGAAAAAAGG  
 AAAAAAAGGGCGGCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
 TTGGCCGCATGGCCCACTTGTATTATGACG

09978193.101541

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTRAPWKEKSQLERALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL  
LLLLKLHLWPLRLPADLAFVRLALCKKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFRFSYSEAEERESNRAARAFRLALGWDWGPDPGSDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGDGGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGVPVPGYLLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRVLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSILIRYDVTTEPIRDPQGHCMATSPGEPGLLVAPVSSQSFPLGYAGGPPELAQGGK  
LLKDVFRPGDVFFNTGDLVCDQGGFLRFHRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486

## FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
GCTTTGCCATCTCCCTCCGGGGGAGCCGGCGCGCTCCACACCTTTGCGGCACATCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTTCTGCGGCTCGGAACCTCGATTGACGCTCTGAACCC  
CCATCGTGGTTTTTTTAAACACTTCTTTTCTCTCTCTCTCTGTTTGGTTGACCGTTTCCA  
TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCTCGG  
CTGGCAGAAGGGGTGACGCTGGGCAGCGCGGAGGAGCGCGCCGCTGCCCTTGGCGGGCTTT  
CGGCTTTAGGGGCAAGGTGAAGAGCGCACCGCGCGTGGGGTTTACCGAGCTGGATTGTATG  
TTGCACCATGCTCTTGGATCGGGGCTGTGATTTCTCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCCAGGCGTACGGTGCC  
AAGGGATTACGCTTGGCGGACATCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAA  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGTACTACACTGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCCTGGAACGGATGTTTACGCTGATAAACCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACAGCTCAAGGCATTTGGAGACGTGCCCC  
GGAACTGAAGATTAGGTTTACCGCGCCTTATGCTGCCAGGACCTTTGTCCAGGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAAACGAGTTTCCAAGTCAAGCCACCCAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCTACTGTGCGGGCTTCCCAGTGTAGGGCCCTGCA  
ACAACTACTGCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGTCATGGACCCGATAGATGTCAGATTTCGAAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAAGGTCTTTCAGGGATGTGGTCAGCCCCAAACCTGCTCCAGCC  
CTCAGATCGCCCGCTCAGCTCCTGAAAATTTTAAATACAGTTTCAGGCCCTACAATCTGTA  
GGAAGAGCAACAACTGCTGCAGGCCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCTTACCTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCGAGGTGGATGTGGACA  
TCACTCGGCTGACACTTTTATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAA  
CTAAAAACGCTTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGTATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTTCCACCGAGTTTGTGTTTGTACCA  
CAGAGGCCCGCGAGTGGATCCCGACCGGAGAGAGGTGGACTCTCTGAGCCCGAGCGTGGC  
CACTCCCTGCTCTCTGGTCTCTCAGCTGCATTGTCTCTGGCAGTCAAGAGACTGTGTCAGATA  
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTAGCTATCTGAATGCGCAACTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCCCAAAAAATTACCGTTTTCATGAGAAGAGAG  
CAGTAATGCAATCTGCTCCCTCTTTTGTCTTCCCAAAGAGTACCGGGTGCCAGACTGAACCTG  
CTTCTCTTTCTTCACTGATCTGTGGGACCTTGTATTATCTAGAGAGAATCTTACTCAA  
ATTTTTCGTACCAGGAGATTTTCTTACCTTCAATTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCAGTTGTGAGGGTTTTTTTTTCTCATTAAAAAT

0978493.101504





# FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGACCGCGCGCGGGG  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGTGCCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCGAGAAACGGCTTCTTCTCCTCACTTCGCCGCTGTGTGATGTGCGGGAGAGATTGGCAAACGCTCTAGG  
AAAGGACTGGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGAGCGCTCCACTTCGCAGTTCTTTCAGGTTGTGGGGACCGCAGGACAGACGCGCGA  
TCCCGCCGCCCTCCGTACCGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGCGCCACGA  
AAAGTTCTGTTCCTCACTGTGATTCCTCAATTCTTGCTTGGTTTTTTCTTCAGAGAACTTTTGGGTGGAGATTA  
ACTTTTTTCTTTTTTTTTTCTTGTGGGAAGCTGCTTAGGGGGGGAGGAGGAGAAAGTGAATGTGC  
TGGAGAAGAGCGAGCCCTCTTGTCTTCCGAGTCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGTGACAGCTGAGAGGAGAGGAGGATTTCTTCGCGAGTGGAGAGTCTTACCGCTCTGTGGGTGCATG  
TGTGCGCCCGCAGCGCGCGGGGCGCTGTGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGCTCCCA  
GGGGCTCTCGGGGCACTCGCCTCGCCTCTTCCACAGGCTCTGTGTCTGCTCGGAAAGATGCAACGATGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCTCTCACTTATGGTTACCTGTCTGGGGCGAGGCTTAGAAGAGGAGG  
AAGAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCAGCCCATCTCA  
TTTTTCATCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAAGCTCGCTGCCGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTTCACACCATCCAGGAGTCAGT  
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTTCTATATAGACCTTACCCAACTCACTGTTTATC  
CTCTGGAACAATGCCACCTTCACTCAGAACTGAAGGAGTTGGATATTCAACGCATATGTTGGGAAAAATGGCACT  
TGGGTTTTTAAACAGAAAAAGATGATGCCACAGAAAGAGGATTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAACGACAAATGCTG  
CCTGGGACTATGACAAATGGCATATATCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT  
ACCCCAACAAAGCCTATATTTTTATATCTGCTATCAAGCTGTTTCACTTACCACCTGCAAGCTCCTGGCAGGTATT  
TGAACACTACCGATCCATTATCAACATAAAGAGAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA  
TCAACAACTGACATTGGCTCTAAAGACTTATGTTTCTATAACAAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCTTACGGCAGGAGGAGTAACTGGCTTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGATCC  
GGGCTGTAGGCTTTGTGCTAGCCCACTTCTGAAAAACAAGGGAACAGTGTGAAGGAACCTTGTGCACATCACTG  
ACTGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATGTATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAAGTGAGGGTCTTGCCTCACCCCGAGTAGATATTTTGCTATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCTTGGGACGAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGACGCACTG  
GAAATGCTTACAGGAAATCTTGGCTACAGCGAGTGGGTCCCCCTCAGTCTTTTACAGCACTGGGACCGAAACG  
GTGGCAATGAACGGATCACCTTGTCACTGGCAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGTGTGACCTATCTAACAGGTATCAGGAATCTGAGAGAGCTCTCAGAGGCTCTCAGATTCAACAAAC  
TGCAGTGCCTGTCAGGTATCCCCCAAAGACCCAGAAGTAACCTTAGGCTCAATGGAGGGGTCTGGGACCATG  
GTATAAGAGAAACCAAGAAAAAGGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAGCAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGTAAACAGCAAAATTTGGCTCGATAATATCGCTGCCTAAGCGTCA  
GGCTTGTCTTATGCTGTGCCATCCAGAGACTTGTGCCCTTGGCCGACACATGAAACTGTCTGCTCAGTG  
CCAAGGTGCTACTCTTGACAGCCACCTTAGAGAGAGTGAGATGTTTATTTCTCTGCTCTCTTAGAAACGCTG  
GTGAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAAACATGCTTTGAATTATAGGAGGAGAAACATA  
ACCTACCATCGCAAGCTGTCTAATTTGATGGAAGTTACAGGTTAGCATGATTAAACACTCCTTTGATAAATTAC

097673-101541

0 9 8 7 6 5 4 3 2 1

[illegible]

## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296  
><subunit 1 of 1, 515 aa, 1 stop  
><MW: 56885, pI: 6.49, NX(S/T): 5  
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCPLDNLATLPQKLKEVGYSTHMGVGNHMGFNRKEC  
MPTRRGFDTFFGSLLGSGDYIYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPCTKPIFLYTAYQAVHSPAQAGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA  
LKTYGFYNNIIIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGFVHSPLLKNKGTVCK  
ELVHITDWWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRDTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

007003-16504

## FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCCGAGAAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTCGGGAACCGGCCAGTGC AAGGCATCAGGGTGTGTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCACTATGGAACATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAAGTTGGTGAAGTGGTGGGACCAACAAAT  
GCAGATGCTTTCCAGGATACACGGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCGGCCATGCCAACACAGATGTGTGAATACACACGGGAAGCTCAAGTGTCTTTGCGCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA  
ACTGTCACTAGTACAGCTGTGAAGACACAGAAGAAAGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTACTGCAAATGTCCACA  
TTGGTTTCGAAGCTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCGAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCCTTCAAGTG  
TAAATGCAAGCAGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTTCTG  
TGAAGGAAGTCTTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAAGGCAAAATTAATAATGTTACCCAGAACCCACAGGACTCC  
TACCCCTAAGGTGAACCTTGCGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCGAGCTTCAATCATGGGATCTGTGACT  
GGAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAAGACATTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAACATGCCCTGGCATGGGAGAG  
ACACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATCAGTTGTATCAAGGAACTGATGC  
TACCAAAGCATCATTTTGAAGCAGAACGTGGCAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTCAGGCCTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTTATATTGACTTTGTATGTGAGTTCCTGGTTTTTTTGTATATTGCATCATAG  
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTTGTAATGTACCAACAGAAAATATTATG  
TAAGATGCCTTTCTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTCTTA  
GAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGGA  
AACTATGACATCAAAGATAGACTTTTGCCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAAATCTTTGTAATAATAA

09578493.101504

## FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE  
ATCEPFGCKFGEVCVGNKCRCPGTYGKTCSDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRVCVNTFGSYCYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

0970193 101501

## FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGCTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCCC  
AGAAATGGGAGCTGACTGATATGGTGGTGGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT  
GAGCTGGAAGGGTGAAAGAAGATGCCTAGAGAATGGCAATTTAAAGAAAAAGATATACT  
TGTTTTGCCCCCTGACCTGACCGACACTGGTTCCTGAAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAAGTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCGAGACCTGTGCAATCAATAATGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCACACAAGATGACAAACAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTTAAGACAAAACTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTTGCTTCCACATGGAATGAAATAAAAAATAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

007673-10454

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVVVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMDTSLDVYRKLIENLNLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP  
VQSNIVENSLAGEVTTIGNNGDQSHKMTT SRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

007313-10551



# FIGURE 48

GCGACGTGGGCAACCGCCATCAGCTGTTTCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
 GGGCTGTTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCCG  
 TTGCATCTTCTACACATACAGCTATTGTTAGGTTGCGTGGGACACGCTGGGCTCTGTCC  
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCTGGATCCTGTTT  
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACTATGCTATCAACGTGAGCCTGAT  
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCCACTGAGCCCTCA  
 ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCGTGTG  
 GACAGCGTGGCCCCCGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCG  
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
 CTGGGTCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
 GCTGCCCTGCAGTTGCCCAGGGCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
 GCAGCTCGCCCAACCCACGACCCACACACCCCTCTGCTGCCCCAGCCCGCCCATCGCTTCC  
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCACTGATGCTCCTGGGACC  
 CTACGCAATCTGCGCTGCGTCTCATCAGTGCGCCACATGTAACCTGATCTACAACAGCT  
 GCACCAGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG  
 GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGCCCTGTGCTGTGCTCGAGCCTGACGGA  
 CACTGGGTTTCAAGCTGGCATCATCAGCTTTGTCATCAAGCTGTGCCAGGAGGACGCTCCTGT  
 GCTGCTGACCAACACAGCTGCTCACAGTTCTGTGGCTGCAGGCTCGAGTTTCAAGGGGCGAGCTT  
 TCCTGGCCCAAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCATGGCCCTGGGAGGCCAGGCT  
 GATGCACCAAGGACAGCTGGCTGTGGCGAGCCCTGGTGTGAGAGGAGGCGGTGCTCAACTG  
 CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAAG  
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCTGAGGGGGG  
 CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
 TCTGCTGCCCTATCCTGACCAACCACTGCTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
 GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCTCCTGGGGCCCTAG  
 GGCTGCGAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGATGG  
 TGTGTACCAAGTGTGTGGGTGAGCTGCCAGCTGTGAGGGCCGTGCTGGGGCACCACTGGTG  
 CATGAGGTGAGGGGCACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
 CCCCAGGCGCGCGGTCTTACCGCGCTCCTGCTATGAGGACTGGGTGAGCAGTTTGG  
 ACTGGCAGGTCTACTTCGCGAGGAACCAAGAGCCGAGGCTGAGCCTGGAAGCTGCTTGGCC  
 AACATAAGCCAACCAACAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
 AGGCAGGCAAAATGGCATTACTGCCCTGTCTCCCAACCTGTGATGTGTGATTCCAGGCAC  
 CAGGCAGGCCCAAGGCCAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA  
 CTCCCCACCTGCGAGGACAGGGGTGTCTGTGGACACTCCCAACCCAACTCTGCTACCAAGC  
 AGCGCTCTCAGCTTCTCTCTCTTACTCTTTAGATACAATCAGCCAGCCAGCTGTGTT  
 TGAATAATTCCTTTTTTGGGGGGCAGCAGTTTCTTTTTTTTAACTTAAATAAATTGTTTAC  
 AAAATAAAA

0978193.101501

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWFWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPITHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPQCGDSGGFVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGALVSEEAULTAAHCFIGRQAPPEWSV  
GLGTRPEEWGLKQLILHGAYTHEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPGERG  
WVLGRARPGAGISSLQTVPTLLGPRACSRLLHAAPGGDGSFILPGMVCTSAVGELPSC EGLS  
GAPLVHEVRGTWFLAGLHSGFDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE  
GSCLANISQPTSC

**Important features:**

**Signal peptide:**

amino acids 1-15

**Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

**N-glycosylation sites.**

amino acids 37-40 and 564-567

**Kringle domains**

amino acids 79-96, 343-360 and 235-247

## FIGURE 50

CGGGCCGCCCCCGGCCCCATTGCGGCCGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGAGCCTTCCACCA CGGGGAG  
CCCAGCTGTGAGCCGCTCACAGGAAGATGCTGCGTGGCGGGGAGCCCTGGCATGGGTGT  
GCATGTGGGTGACAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGTCTCTCTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAACA  
GCTGGTGACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCGGACCTGTGCGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCG  
GACGAGGGCAGCTTACCTGTCTCGTGAGCATCCGGGATTTGCGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAAACGA  
GCAGGGCTTGTTGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA  
GCTGCTGTGGTGGCGCAACCCCGTGTGTCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG  
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGTGTGTGTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTGCTGGAGAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCTGAGCCTATGAGGACCAGG  
GAGCTGTACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCTGTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACGTGCAGCCTTATTTCTCAATGGACATGATTCCTCAAGTCATCCTGTCTGCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC  
TTCTTCCAGTGTGCGTGGACATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA  
CTGACTGACCCCTGCCTTATTTTACCAAAGACAGATGCATAGTCACCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT  
CTTCTCAGACAGGACAGTGGCGCCTCAACATCTCCTGGAGCTAGAAGCTGTTTTCCTTTC  
CCCTCCTTCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCAGGAATGCTTTGGGGACACCG  
AGGGGATGCCCCCACCACCACCATGTTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC  
TTGCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCTCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTAAATGTGGGAC  
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAAATAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA

## FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQVPL  
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED  
DGQEIA

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

0076193.101501

# FIGURE 52

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCCTTCTAAGAAGGGGGAGTC  
 CTGAACTTGTCTGAAGCCCTTGTCCGTAAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
 AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCCTTGTCTCAGCAACATGAGGCTTTTCT  
 TGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
 GAAGTGAAAAATTGAAGTTCTCCAGAAGCCATTCTATCTGCCATCGCAAGACCAAAGGAGGGGA  
 TTTGATGTTGGTCCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTTATTTCACTCCACTC  
 ACAAACTATAACATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
 TGGGACCAAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAGCTCATCATCTCTCTGTC  
 TCTGGGCTATGGAAAAGAAGGAAAAGGTAAATTTCCCCAGAAAGTACACTGATATTTAATA  
 TTGATCTCCTGGAGATTTCGAAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT  
 AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
 ACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAG  
 AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
 TAGAGATACATCTACCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCGAGTCATCTTTAA  
 AGAATTTTATTTTATACAAATGTTCTTTCTGCTTTGTTTTTATTTTATATATTTT  
 CTGACTCCTATTTAAAGAAGCCCTTAGGTTTCTAAGTACCCATTCTTTCTGATAAGTTATT  
 GGGAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTACAG  
 ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCACTGGGAATATACC  
 ACGACATGAGACCAAGGTTATAGCACAAATTAGCACCCTATATTCTGCTCTCCCTTATTTTCT  
 TCCAAGTTAGAGGTCAACATTTGAAAAGCCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
 GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACGAGGAAAA  
 TGGTTGTTGGACCTGACTTGTGTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
 TTAGAAAACAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAAATCCAGCACTTTGGGAG  
 GCTGAGGCGGGCGGATCACCTGAGGTGGGAGTTGAGACCAAGCCTGACCAACACGAGAAAA  
 CCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGTATGCGTGCTGTAATCCAGCT  
 ACCCAGGAAGGCTGAGGCGGCAGAACTACTTGAACCCGAGGCGGAGGTTGCGGTAAAGCCGAG  
 ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACACGGTTAATACCATATNA  
 ATATGTATGCATTGAGACATGCTACTAGGACTTAAGCTGTATGAAGCTTGGCTCCTAGTGAT  
 TGGTGGCTTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAATG  
 TATCAATATGTTTATAGATGAGGTAGAAAGTTATATTATATTTCAATATTACTTCTTAAGGC  
 TAGCGGAATATCTCTCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
 TTGTATCATAAGATAAAGTAGTAAACCAAGTCTACATTTTCCATTCTGTCTCATCAAAAC  
 TGAAGTTAGTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG  
 TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAAATGGTGAACCTTGTCTCTA  
 CTAATAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCAGCTACTCGGGAG  
 GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
 ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGAGCAGA  
 CCTACAGCAGCTACTATTGAATAATACCTATCTCTGAGTTT

0978193.101504

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 24172, pI: 5.99, NX(S/T): 1  
MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNQPIWFTLGILEALKGWDQGLKGMCVGEKKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDALVED  
IFDKEDEKDGFIISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

09078193-101504

# FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCCTTTGAAGTACATCCGTGCATTTTTTTTAGCAT  
 CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA  
 CTAACATCTCAGTCTCTGAAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC  
 CTGCCACCCCTCAACGTCCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC  
 TACACAGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
 TGAGGAGATGTTCTCCAGTTCCGCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTTCAAG  
 ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG  
 CAGCCCGAGGATGAGGGGATTTACAACCTGCTACATCATGAACC CCCCTGACCGCCACCGTGG  
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
 CCGTGATGTGGGTGCCTCCGTGGGGGCTTCTGGCTGTGGT CATCTTGGTGCTGATGGTG  
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGC CAAGTAGTGGGTGGCCGGCC  
 CTGCAGCCTCCCGTGTCCGCTCTCCTCCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCG  
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCCTCTGAACCCCCG  
 ACTTCGTATCTCCACCCTGCACCAAGAGTGACCACTCTCTTCCATCCGAGAAACCTGCCA  
 TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG  
 GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAAGGAGTGGGTGGGCAGGGGTAGA  
 GGAGGGGCCGTGTACCTGCCAGTGCTTGCCTGGCAGTGGCTT CAGAGAGGACCTGGTGG  
 GGAGGGAGGGCTTTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCCTGGCACGGCTG  
 TGCTCCTCCCCTGCTCCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTCTGA  
 AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCAGGGGCATGACGGAAAGCCAGGG  
 CTGCAGGCAAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
 GCTAGTGGCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC  
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
 GCTCTGCCCTTCTCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
 GAGGAGGCCATGCACAGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAATCTCCCAGTT  
 GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG  
 GCATAAGGGGAGGCCTTGAACCTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG  
 CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
 ACAGTGGCTCAGCCTGTAACTCCAGCACTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
 CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAATACAAGAATTAGCTGGCGGTG  
 GTGGCGTGTGCTGTAAATCCAGCTATTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTATAGTGCCATGCAATTGACGCTGGGTGAC  
 ATAGAGAGACTCCATCTCAAAAAA

0978193 10.504

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

0073193 105001



## FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG  
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCC

0973193-14504

## FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCTCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

0978193.102501

# FIGURE 58

TGC GCGACCGCTCGTACACCATGGGCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCCTCCTGT  
 TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCGCGCCGAGCTCACCCCCAGTGGTCTGTGCTCC  
 CTGGTGATTGGGTAAACCACTGGAAAGCAAGCTGACAGCCGACAGTGGTGCACTACTCTGCTCCAAAGAGA  
 CCGAAAGCTACTTTCACAACTGTGGCTGAACCTTGAAGACTGCTGCTGCTCATCTATTGCTGCTGGATTGACATA  
 TCAGGCTGGTTTACAAACAAACATCCAGGGCCACCCAGTTTCTCTGATGCTGTGGATGTACGTGCTCCCTGGCTTTG  
 GGAAGACCTTCTCACTGGAGTTCTCTGGACCCAGCAAAAGCAGCGCTGGTTTCTTATTTCCACACCACTGGTGGAGA  
 GCCTTTGGGGCTGGGGCTACACACGGGGTGAAGATGTCCGAGGGGCTCCCTATGACTGCGCGCGAGCCCCAAATG  
 AAAACGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCGCTGGTGTG  
 TGGTTGCCACAGTATGGGCAACATGTACAGCTCTACTTTCTGAGCGCGAGCCGAGGCTGGAAGGACAAAT  
 ATATCCGGGCTTCTGTCTACTGGGTGCGCCCTGGGGGGGGCTGGCCAAAGACCTTGGCGTCTCTGGCTTCAGGAG  
 ACAACAACCGGATCCCACTCATCGGCCCTTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACAGCTGGC  
 TGCTGCCCTACAACATACATGGTCACTGAGAAGGTGTTCTGTGAGACACCCCACTCACTACACACTGCGGG  
 ACTACCGCAAGTCTTTCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGAGGACACAGAAGGGCTGGTGG  
 AAGCCAGATGCGACCTGGCGTGCAGCTGCAGTGCCTCTATGTTACTGGCGTCCCCACACAGACTCCTTCTACT  
 ATGAGAGCTTCCCTGACCGTGACCTTAAATCTGCTTTGGTGACGCGATGGTACTGTGAACCTTGAAGATGCCC  
 TGAGTGCCAGGCTGGCAGAGCCGCGAGGAGCACCAAGTGTGTTGCTGCGAGGAGCTGCCAGGACGAGCATCG  
 AGATCTGGCCACGCCACACCTGGCTATCTGAACCTGTGCTCCTTGGGGCTTGAACCTCTGTGCCACAGGA  
 CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCTCTGGGGCTGTGATGGCCACAGCGTTTTGCAAAAGTTTGTA  
 CTCACCACTCAAGGCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCTCTTCTCT  
 GTGGCAGTGAAGAGGAAGAAGATGAGAGTCTAGACTCAAGGACACTGGATGGCAAGATGCTGCTGATGGTGA  
 ACTGCTGTGACTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCAGTCCCTGGCTGGGGCCATG  
 TGTCCCTCTATTCTCTGGGCTTTTCATACITGCTTACTGGGCCCTGGGCCCGCAGCTTCTCTATGAGGGATGTT  
 ACTGGGCTGTGGTCTGTGATCCAGAGGCTCCAGGGATCGGCTCTGGGCCCTCGGGTGACCTTCCACACACCA  
 GCCACAGATAGGCTGCGCACTGGTCTAGTGGTAGTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
 TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCGAGCAGGGGAGTTGTTGTGGTTCTTCTGGTTCAGGCG  
 CCTGGGACATCTCACTCCACTCTACCTCCCTTACCAACAGGAGCATCAAGCTTGGATTGGGAGCAGATGTG  
 CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGGCCAGGATGAAGCTGTC  
 CTCCTTCAACCTGGGACTGTGGTTCCAGGATGAGAGCAGGGTGGAGCCATGGCTTCTGGGAACCTATGGA  
 GAAAGGGAATCCAAGGAGCAGCCAGGGCTGCTGCGAGCTTCCCTGAGCTTGGACCTCTTGCTAACCCACCATCA  
 CACTGCCACCTGCTAGGGTCTCACTAGTACCAAGTGGGTGAGCAGGGCTGAGGATGGGGCTTCTATCCAC  
 CCTGGCCAGCACCAGCTTAGTGCTGGGACTAGCCCAAGAACTTGAATGGACCTGAGAGAGCCAGGGGCTCCC  
 TGAGGCCCTTAGGGGCTTCTGTCTGCCCCAGGGTGTCCATGGATCTCTCTGTGCGAGCAGGCTGGAAGT  
 CAGGGCTGCTTCTATGGCACTAGGCTCTAAGTGGGTGACTGGCCACAGGCGAGAAAGGATACAGCTCTAGGT  
 GGGGTTTCCAAAGACCTTCAAGCTGAGCTGAGCTGCTCTCCACAGGGTTCTGTGCACTGGAATTTCTCTG  
 TTGCATACATGCTGCACTGTCTCCCTTGTCTCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
 GATTCTGGCAATAAAGTCTCTGGATGCTGTAAAAAAGGAAAAAAAAAAAAA

0978193.101504

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVVRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVVFQTPPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTNVLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

**Important features:**

**Signal peptide:**

amino acids 1-28

**Potential lipid substrate binding site:**

amino acids 147-164

**N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

**Lipases, serine proteins**

amino acids 189-201

**Beta-transducin family Trp-Asp repeat**

amino acids 353-365

## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGACGCGCGGCGACGGCGACATGGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACC AAC  
CAGTGGGCAGTCACCAACCCGAGGACGTGCTGTGGGGGCGGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCCTCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAAGCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCCCCTGGACTTTCCTCATCAGCCTCCTGGAACTGCCA  
GCCCCCTCTTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAAATGA  
CCTCAGCCCCGCTGCAGTGCGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGCGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTTGCCAAAG  
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACCAGGCTCTGTGTCTCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGCCACCACCCTGTGCCGGT  
GGCTCTGGGTGCTTCCGCTGGTGTGAGGGCGGGCTGGTGTCTATGGCACTTCTCCTCTG  
CTCCACCCCTGGCAGCAGGAAGGGCTTTGCCCTGACAACCCAGCTTTATGTAATAATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGTGCCCCATGGCTCCCAGACTCTGTG  
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGTGTTTGGAGAGC  
GAATAAATGTTTTCTCATTCAAAG

00733-10334

## FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYEGEGYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDILLFSALWTFWLVFGFC  
FLTQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPFFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

0978193-101504



## **FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDEAEPEGMFACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRIGT  
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLMLSPVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGGQVLRKGPDLHASSCLWHLQGPKDLM  
KLRLLEWTLAECDRLAMVDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSSTPYFPSSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIONRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNLGCVFACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDGQPDCLNGSDEEQCEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD  
CGLQGPSSSRIVGGAVSSEGEWFWQASLQVRGRHICGALIAIDRWVITAAHCFQEDSMASVT  
WTVFLGKVVQNSRWPGEVSVFKVSRLLHHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 46-67

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

#### **N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### **Kringle domains.**

amino acids 746-758 and 592-609

#### **Homologous region to Kallikrein Light Chain:**

amino acids 568-779

#### **Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567



## **FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACC GGCCCGGTGTGCGGTGCACTATGGCTTGTAACAACAGTCGGACCCCTGCC  
CTGGAGAGTTCTCTGTTCGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGACAGGCCACATTCCAGTGCAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAAGAAGCCCAACCCGACGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGTGTCAGCTCGACCACCGGTGGTGCCTCGGCCGCGTGCAGCC  
CGTCTGCCTGCCCGCGCTGCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAAGT  
ATCCACAGGACCTGTGTCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGCGGGGCTGGTCACTGGGGCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAATGCCCCCTGCAAAGCAGGGCCCACTCCTGGACTCAGAGAGCCAGGGC  
AAGTGCCAAGCAGGGGGACAAGTAT

0976193-104504



## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFPGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDVAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

007000-100000



## FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCDGVDACGDGSDAAGCSSDPFPGLTPRP  
VPSLPCNVLTLEDFYGVFSSPGYTHLASVSHPOQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSGWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSD EWDCS  
YVLPRKVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRLSLQLRQDMTPGGGPGARRRQGRRLMRLRVR  
RLRRWGLLPRNTTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTIVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAV  
LALEDEDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

## FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAGAAGTTTGTAATTTTTATATTACTTTTGTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

0070193-101501

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

#### **Potential type II transmembrane domain:**

amino acids 26-42

#### **Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

#### **Leucine zipper pattern**

amino acids 78-99 and 85-106

#### **N-myristoylation site.**

amino acids 110-115

#### **Ribonucleotide reductase large subunit protein**

amino acids 116-127

## **FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAAC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTGGAAGTCACCGTTATCTTATTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

0070403-103504



**SECRET**

CAGCCCGCGCGCGCGCGCGAGTCTGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
 CTGGGCGCGCCCCCGGGCCCCGCGGTGGGCATGGGCGCACTGGCCCGGGCGCTGCTGCTGC  
 CTCCTGCTGGCCAGTGGCTCTGCGCGCGCCCCGGAGCTGGCCCCCGCGCCCTTACGCTG  
 CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCC  
 TGCCGAGCGCCACGCGCAGCGCTTGGCGCTCGCCCTGGAGCCTGCCTTGGCGTCCCCCGCGG  
 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
 CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
 TAACTTTGCGGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
 CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG  
 GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAA  
 CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGGCCTGGGATTAAATGGAATGGAATAC  
 TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
 CTGGTGACACAAGCAAACTCCCAAGTTTTCTCATGACAGTGTGTGGAGCGGGCTTGCC  
 CGTTGCTGGATCTGGGAGCAACCGGAGCTTGTCTGTCTTGGGTGGAATTGAACCAAGTTTGT  
 ATAAAGGAGACATCTGTGTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAATTTCT  
 AAATTGGAAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
 CATCGTGGACAGTGGCACCACGCTGCTGCGCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
 AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
 CTGGCGTGTCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
 GAGAGACGAGAACTCCAGCAGGTATTCCGATACACAATCCTGCCTCAGCTTTACATTACG  
 CCATGATGGGGGCGGCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCATCCACAAAT  
 GCGCTGTGTGATCGGTGCCACGCTGATGGAGGGCTTCTACGTCTCTCGACAGAGCCCAGAA  
 GAGGGTGGGCTTCGACAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
 CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
 CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTGTCTT  
 AATCGTCTCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTGACCTTGAGGTCTGCA  
 ATGATGAGTCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCGCTGACACTCAAGCAA  
 CCATGAACCTCAGCTATTAAGAAAATCACATTTCCAGGCGACGACGGGAGTCTGATGGTGGCG  
 CTTTCTCTGTGCCACCCGCTTTCAATCTCTGTCTGCTCGACAGTGCCTTCTAGATTAC  
 TGTCTTTTGATTCTGATTTCAGAGCTTTCAAATCCTCCCTACTTCCAAGAAAATAATTA  
 AAAAAAACTTCATTCTAA

## FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPSPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSSTYRSKGFVTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR  
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIVLRDENSSRSFR  
ITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWLWIVSYALMSVCGAILLVLLVLLLPFR  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310



09/01/2013

&lt;subunit 1 of 1, 377 aa, 1 stop

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNNEVIFMALDLASLASVRFAFAFLSSSEPRLDILIHAG  
ISSCGRTREAFNLLLRVNHIGPFLLLTHLLLPCLKACAPSRVVVVASAAHCRGLRDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSSELFRLHVPGLRPLLR  
AGLVLRLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL  
PLAGLPGEDAEPDEDQSEDEAPSSSLSTPHPEEPTVTSQPYPSQSSPDLKSMTHRIQAKVEP  
EIQLS

### Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

## Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

# FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCTCATCATGGAGGACATGGCTCAG  
 GACTCCCCCGCCAGATCCTAGTCCACCCAGGACAGCAGTGTTCAGGGGCCCTGGCCCTGCCAGGATGAGCTGC  
 CAAGCTCTCAGGCCAGCCACTCCACCATCGCTGGTTGTGATGGGAGCCCTCGACTGAGTGGCCCCAGAC  
 CCACACCACTCTCTGCCTGATGGGACCTTCTGCTGTCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACCGGCACTGACAGAGGCCCT  
 CGGCTGTCTGTGCTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGCCGCCCTGGGGCCACCCAGAGCCCAAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
 GCCCTCAGGCCCGGAAGGCAACAAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
 ACCTACATGTGTGTGGCCACAACAGCGCGGTGTGGCTCAGCTGGAAAGTCACTGGCCCTGTCTGCGCCCTCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCGTGGGCGAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCCGACAGACTTGGAGGCCCTCACTGGGGCCAAAGACTACGAGTTCAAAGTGAGACCATCTCTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGTCTCTGAGGCTGCCGAAAAAGTGCCCAAGTGCCCACTCAGGAA  
 GTGACTCTAAAGCTGGCAATGGCACTGTCTTGTGAGCTGGGTCCACCACTGCTGAAAAACCAATGGCATC  
 ATCCGTGGCTACAGGCTGTGGAGCTGGGCAACATCACTACTGCCACAGCCAACTGGACTGTAGTTGGTGAGCAG  
 ACCCAGCTGGAATCGCCACCCATATGCCAGGCTCTACTGTGCGTCAAGTGGCTCAGTCACTGGTCTGGAGCT  
 GGGGAGCCCACTAGACTGTCTGCTCTCTTTAGAGCAGGCCATGGAGGAGGCCACCAAGAACCCAGTGAGCAT  
 GGTCTCTGAGCCTTGAGAGCTTGAGGCTACCTTGAAGCGGCCCTGAGGTACTTGGCACTTGCCGCTGTGCTC  
 TGCTGTCTGTCTTGAGCAACCGCCGTGTGTATCCACCGCCGGCCCGAGCTAGGGGTGCACTGGGCCCAAGTCTG  
 TACAGATTAACAGTGAGGATGCCATCTAAAAACAAGGATGGATCAAGTGACTTCCAGTGGTGGGAGACAT  
 TGCGGTTCCACCTCTGCTCTCTCGGACCTGAGCAGCAGCAGCAGCTCAGCAGCTCGGCTGGGGGGGAGTCCCGG  
 GAGCCACTTAGACTGTCTGCTCCCTTGTCTCTCTGGGACTCCCGAAGCCCGGCGTGCCTCTCTTCCGATCC  
 AGCACTTATTTAGGCTCCCTCATCTGCTGAGCTGCCCTCCAGTATCCCAAGCCAGGCAAGTCCCGAGTCCGAGT  
 GTGAGCGCCTCCACCCCACTGCTGGCCAGCTCTCCAGCCCTGTTCAGCTCAGACAGCTCTGACAGCCAGG  
 GGACTCTCTCTCCCGCTGTCTCTGGGCCCTCGAGAGGCTTGAAGGCCAAAGAGCAGGAGCTGACAGCAT  
 GCCAACAGTTCCTCCACTGCTCCGGGGCAGCCACTCTTGGAGCTCGGGCTCAAGCTTCCAGTGGCTTCC  
 AAGAACCTTTCCAAAGCCGAGGCTGTGCCCAAGCTCTGGTGTCTGGCGGCCCTGGGACGAAACTCTCT  
 AGCTCTCTCAATGAGCTGGTTACTGTCTATCTCTCCAGCAGCCCTCTTCTCTCATGAAACTCCCCCACTCAG  
 AGTCAACAGAGCCAGCTCCGGTGGCCACACAGGCTCCCTCTCCATCTCTGCGCAGCAGCCCCCATCCCCATC  
 CTTAGCCCTCGAGTCCCCCTAGCCCCCAGGCCCTCTTCCCTCTCTGGCCCGAGCCAGCTTCCAGTCCGCTTCC  
 AGCTCTCACTGTATCCTCTGGGGGAGGATCAAGACAGGCTGTGACCCTGAGGAGGTAGCCCTGTCTTGGAA  
 CTCAGTGAGGCTGAGGAGACTCCAGGAAACAGGCTCTCCCATGCCAAGGGCTCTTCACCCCCAGCCACTAT  
 GGGTACATCAGGCTGCCAACAGCCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCAAAGGG  
 GGAATCTTGTGTGCCCACTCGGCCCTGCTCACCCCACCCCGAGCGAGGCTCTTAGCCAAATGTTGGGGC  
 TCAGCCTCGAGGACAAATGCCGCGCCAGCCAGCCAGCCTGTGCTCAGTCTCTCOGATGGCTCTTCTCTGCTGAT  
 GCTCACTTTCGCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCAGGAGGGCAGACTGC  
 GTCTTATAGATGCTCTCACTCTCTCCCAAGGGATGAGATCTTCTGACCCCCAACTCTCTCCCTGCCCTTG  
 TGGGAGTGGAGGCCAGACTGTGTTGGAAGACATGGAGGTGAGCCACACCCGCGCTGGGAAGGGGATGCTCCC  
 TGGCCCCCTGACTCTGAGTCTCTTCCAGAGAAGTCACTGCTGATGCCAAGGCTGGTGTCTCTCTCT  
 GTAGATTACTCTGAAACCGTGTCCCTGAGACTTCCAGAGCGGGAATCAGAACCCTTCTCTGTCCACCCACAAG  
 ACTGGGCTGGTGTGTGGGCTTGTGGGCTGTGTTTCTCTGAGCTGGGGTCCACTTCCCAAGCTCCAGAGAG  
 TTCTCTCCCTCAGGATTTGTAAGAACAAATGAAACAAATTAGAGCAAGCTGACTCTGGAGCCCTCAGGAGCAAA  
 ACATCTCTCAACTGACTCTCTAGCCACTGCTTCTCTCTGTGCCATCACTCCACCAACCAAGTTGTTTGGC  
 CTGAGGAGCAGCCTGCTGCTGCTCTTCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTTGCTTCT  
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCTCTCAGCCTTACCT  
 GGGCCCTCTCTAGAGAAGAGCTCAACTCTCTCCAACTCACCATTGGAAGAAAAATAATTATGAATGCCACTG  
 AGGCAGCTGAGGCCCTCACTCATGCCAAACAAAGGGTCAAGGCTGGGTCTAGGAGGATGCTGAGGAAAGGGGAG  
 TATGAGACCGTAGGTCAAAGCACCATCTCTGTACTGTTGTCACTATGAGCTTGAAGAAATTTGATACATAAAAT  
 GGTAAAAA

00070003.100501

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDLFQGGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQQTLECGPPWGHPEPTVSWWKDGKPLALQPGRHVTVSGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVS IQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLLRLEKVPSPAPPQEVETLKPNGTGVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSQVPAVRRLFPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGSPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPDSQISSQRSQLHCRMPKAGASPVVDS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

# FIGURE 78

CTCCCCAGGTGTCCAGCGCCCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCCCAGAGGAAATCAGCGGGTTCGAGGGGACACTGTGT  
 CCCTGCAGTGCACTACAGGGAAGAGCTGAGGGACCAACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAGGCCAGAGACAAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA  
 ACCTCACCTTGCAGAACGCTGGGGAGTACTGGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTATCTGATCTCTCTGTTTGTCTTTCCAGGACCTGCTGTCTCCCTCCCTCTTCCAC  
 CTTCAGCCTCTGGCTACAACACGCTCTCAGCCCCAAGGCCAAAGCTCAGCAAACCCAGCCCC  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACACAGCCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCTGCAGGGAGCTCCCGCCCCCATGCAAG  
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCGATGTTCCGCATATCTGGCCCCAGTCTCGTGTGCTGCTGAGCCTTCTGTGAGC  
 CGCAGGCCGTGATCGCCTTCTCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTCTGGCTCTCAGCCTTGACTGCGGAGAAAAGGAAGCC  
 CCTTCCAGGCCCTGAGGGGACGTGATCTCGATGCCTCCCTCCACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAAGCTTTCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCGAGCTCTCCTCTTGCACTGTTTCCA  
 GCCTGACCTAGAAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTTCAATCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA  
 GCAGGCCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
 CTCATGCCCAGTGTGCGACCTGCCTTCTTCCCACTCCAGACCCCACTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTTAAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAAGGCCAGTGGGCTGG  
 ATGAACGCTCACACCCCTTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG  
 TCCAGGCCCTGGTCAAGTCAAGGTGCACATTCAGGATAAGCCAGGACCCGACAGAAAGTGG  
 TTGCTTTTNCATTTGGCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
 AAACTTGGCTCCTTCTTGTCTGAAAGGGTTACTTGCCTATGGTCTCTGTTGGCTAGAGA  
 GAAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTTCGGGGTGGTGGTAAAGTA  
 GCACAACTACTATTTTTTTCTTTTCCATTATTATTGTTTTTAAAGACAGAAATCTCGTGCT  
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT  
 CTCTGCTCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACTTGGCTAATT  
 TTTGTACTTTTATAGAGATGGGGTTTCCACATGTTGGCCAGGCTGTTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCCTGCTCTCAGTCTCCCAAAATGGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTGAGTATGCAAACTTGGAAAG  
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
 TATTTGTTTTGTTGTACTTCTTCACTCTTTTCTTCTTACATAATTTGGCCGGTGTCTT  
 TTTACAGCAATATCTTGTATATAACAATTTGATCTCGCTCTTCCACCTTTTCCACCTTATCGTCC  
 ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAA

0978193.101501

## **FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196  
<subunit 1 of 1, 332 aa, 1 stop  
<MW: 36143, pI: 5.89, NX(S/T): 1  
MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD E SLLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG  
TSQYGHERTSQYTGTS PHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128



## FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCCATTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTACAAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

**096870**

&lt;subunit 1 of 1, 146 aa, 1 stop

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTNPVNPVCRMYCSDLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGCF

Signal peptide:

N-myristoylation site.

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

## FIGURE 82

AGCGCGTCCCCCGGGCCGGGCGCCCGCGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTTC  
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACTCTGCCCA  
AGCTGTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGCCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAACCGGCGCTGGAAGTGTCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCTTCGTG  
TACGCCATCTCTTCGCGAGGTGTGGCCTTTGCAGTGACCGGGCGTGACGACAGTGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCGCGTGGGCTCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGAGCCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCTGTGGGCACAGGGGGCCGACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCGCGGCTTCACACGCGCGCA  
GGTGGAGCTGGCTGAAAGCTGCAGCTGCAAATTCCACTGGTGTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACGACCGCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCAGGGAAGGCCGATAATTAAACAGTCTCCACCACCTACCCCAAGA  
GATACTGGTTGTAATTTTTTGTCTGTTTGGTCTTGGGTCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGCCACCAACCAGGGCTCCCCAAGCCCTGGGCCCTTGTGGCT  
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAAA  
GGTACCAGACTTGATGGAAGTCACACCTCTGGAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTTCATTTTACGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCAACCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCGAGTCACCTTTCACAGCGCTGTCTCCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGCTGTGCCTTTGCAGTCATGCCGAGTCACCTTTCACAGCACTGTTCTCT

0978193.101501

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNDNIAYGVAFSQS FVDVREERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCFKHWCCFVKRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

## **FIGURE 84**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGCTC  
ACCACAGTCTTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGTGG  
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAATCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGCGCCGTGGTTACTGGCTGGGCCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTATGATGC  
TGACACAGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAATGCTGAACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGACGATGTGTA  
TCCTGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCAGCAGACCCAACTAACC  
TCCACTAGCTCCAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTCTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTGGTTTTCTCGATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGSSEEVPGGPWGRVWHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLRLTNASKQTAALGALKKEEVGDCHSCCSGTQACLQTTRAEELGEAQAKLMEQESALR  
ELRERVTVQGLAEAGRGREDVRTLEFRALEAVRLQNNSCPEPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLLVIVGGLDEQGFLTRNTRGRGYWGLRAVRHLGKVGQYQWVDGVSLSFS  
HWNQGEPNDAWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGCGGAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGCTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAAACCCAGCCCGGCCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCGCCGGCCAGCCTCTGGGGGAGAGTCT  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTACCGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCGCCCCCCCTGCGCAGTGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGCGGAGGCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCGCTCCCAGCGGCACCGGGCAGAG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGCTTTGTGGTGCGCATCTGTGCC  
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGAGCCTTACCTTCTCC  
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCTCCAG  
CCACCCGGCCAACCTCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCAGTCTCTGCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCTGCTCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCCGCAACAACGGGAGCCCTGCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGCTTAAGACCAGAGCCCCGAGCCCTGGGGCCCCCGG  
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCGGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCGCGCGGACCATCTCTGCACTGAAGGGCCCT  
CTGTTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCTGCAAGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCTTTCATCG  
TCCAGGGGCTGGCTCCACGTTGCTGAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

><subunit 1 of 1, 331 aa, 1 stop

MENPSPAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRLSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSSPHANSFYYPRLKALPPIARVTLRLRQSP  
RAFIPIPAVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRGLTKSRIVRVQPA  
NNGSPCPLELEESAECPVDCNV

Signal peptide:

amino acids 1-26



[illegible]

GC CGGCGCTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTTGGTGTCCCTGTCTTGC GTGA  
TATTGACAAACTGAAGCTTTCTGTGACCACCTGGACTTAAGGAAGAGTGTACTCGTAGGCCGA  
CAGCTTTAGTGGCCGGCGCGCGCTCTCATCCCCGTAAGGAGCAGAGTCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAAC TA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAGAAGCTCCTAAAGCTTGAGAAAATTTT  
ATCCAACITTTGTTTGGAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCAGAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTCATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGTTTCTCATGATAATGGCAGCCAGTTTTTCTTTCACACTGGGTCGAGCAGATGAAC T  
TAACAATAAGCATAACCATCTTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTTCAAGGGAATTAAGGCTGAAAAGAA  
GAAACCAGAGGAGGAAGTAAAGAAATGAAACCCAAAGGCACAAAAAATTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAATCGAGTTAGTCAGAGCATGAAG  
GC AAAAGCAAAGGTAGTCTGACTGTTTGAAGGATGATCCACTCTCAGTTCTGTTCCAGT  
TG TAGAAAGTGA AAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGTATGAAAAGAACCCTGATGAGAGAAAGAATTGCCAAAAA  
TTAAAAAGGACACAGAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTA AACCGGAACCTTTAGCAG  
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAGCAGAAAAAAGAAGTGAAGGGAAGAA  
GCCCTCCAGATGGTGTGTTGCGGAATACAGAAGAGAAAAGCAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAGAAGGGGAACCTCCCGGGAAGATCAGACCCCTTGCACTGCTGAACCA GT  
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTTCTGAAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTGCATGTACTTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAAGAAGAAGATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCCTGTAACAGGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTGTGCTGGTTTTG  
AAAAACAATTATCTTGTTTGCAAAATGTGGAATGATGTGAAGCAATGCTTTTGGTTACTGG  
TACATGTGTTTTTCTAGTCACTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT  
TCCACAAAAA AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLTKTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKLKLKPGTKNFSLLSFGEAEAEAEAEAEVNRVSQSMKGKSKSSHLLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKCLKKDTSANVKSAGEGEVEKKS  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEAPPDGAVA EYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFSKLTQAI AETPENDIPETEVEDDEGWMMSHVLQFEDKSRKV  
DASMQSDTTFEYIDPRNPVNKRREESKMLMREKKERR

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

## FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCGCCAGGTCGTCGGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGGCGAGAGAAGTGTCCAGACCCATTTCGCCTTGCTGACGGCGTCG  
AGCCCTGGCCAGACATGTCACAGGGTTCTCCTTCGGGTCGGGACTCTGGGCTCCACCACC  
GTGGCCGCCGGCGGGACCAGCACAGGCGCGTTTTCTCCTTCGGAACGGGAACGCTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCAACTCCAGCACTACACTGT  
CTCCTTCAAGTGGTTTGGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCCTCAAGTGGTCACCAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAAGTCTTTTAGGAGTCCCTT  
TCTCCAGACCTCCTCTAGGTATCTCAGGTTTGCACCTCCAGAACCCC CGGAGCCCTGGA  
GGAATCAGAGATGCTACACCTACCCGCTGGATGGAGTCTCGCTCTGTCCGACAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCG  
ATGTACGTCAAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTATCTGTGGGCTGCTTCTTCGTACAGGGCTCTGACTTGGCCGCGCGC  
GAGAAAGTGGTGTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA  
CGACAGCCACGCGCGGGAACTGGGGCTGCTGGACAGATGGCGCTCTGCGCTGGGTGC  
AGGGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTACCCCTGTTCCGCCAGTCCGGC  
GGGCGCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGC  
CATTTCCAGAGTGGCACCCGCTTATTAGACTTTTTCATCACTAGTAACCCACTGAAAGTGC  
CCAAGAAGGTGTCACACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCACCAAGATGAGATTCTTCCAACT  
GAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCAGATGACCTTTGGTGTCTCTGACCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATCACCAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTTCGTGATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCTAGAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCACTCTCAAAGACCTGAGAAGCAGAGGCAATTTCTAAGGGTGGC  
TATGCGAGGAAGGAGCCAAAGAGGGGTTTGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTTGGGGACAAGAGTTCTACCCACCCAGTTTGAAGTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGCATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCCGTGCAAC  
AGCACAGTGTGCTCAGCTCTCCAGCCTCAGGACAACTCTTTTTTCCCTTCTTCAAATCCT  
CCCACCTTCAATGTCTCTCTGTGACTCCTTCTTATGGGAGGTGCAGCCAGACTGCCACTGC  
CCCTGTCACTGCACCAGCTTGGCATTACCATCCATCTGCTCAACTGTCTTCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTGTGACATGGAGCAAACTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCCACTTATCTCCCCCAGGGCCACTCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

## **FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG  
FGTLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLLQKQMHVVGKTIQVFLGVFPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGVRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWQENIA  
AFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD  
PLVLLTQKGVSVPYLLGVNNLEFNWLLFPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

**Important features:**

**Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

## FIGURE 92

GAGAAACAGGCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
 GCTGTCTCTCGTGTCTGGGCGGGTCCAGGCTATGGATGGGAGATTTCTGGATCGAGTGCAGG  
 AGTCAGTGAATGGTCCGCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGA  
 CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
 CAAGGGTGCTCCTGTGGCCACAAACCCAGAGTGCAGAGGTGGAAATGAGCACC CGGGGG  
 GATTCCAGCTTCACTGGGGATCCGCGCAAGGGGAATGCTCCTTGGTGATCAGAGACGCGCAG  
 ATCGAGGATGAGTCACAGTACTTCTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
 CATGAAAGATGGGTTTCTTTCTAAAAGTAACAGTGCTCAGCTTCCAGGCCAGACCCAGGACC  
 ACAACACCGACCTCACTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
 GTCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTACGTCGACACAC  
 GCCAGCCTGGAGCCCGAGCCCGAGGGAATGTCCATACCTGGAAGCCCAAAAAGCGCAGT  
 TCCTGCGGCTCCTCTGTGTCTGTACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGTGAG  
 AACAGAGTCTCTCTCTCGTCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
 GGTGAAGGCTGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCGAGC  
 AGCGAGCCCTGGACTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
 GCAAAACAGGACAGCTCTGGAAGAACCTGGGAACCGGCAGCTCTCTCCAGTACTGGAGGGCCA  
 AAGCCTGTGCTGTGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
 GGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCTCCGGGT  
 CAAGTGAGACGAGGAGGATTCACCTGCCAGCTCGGACCCCACTGGGCTCCGAGCAGT  
 CTCTCTCAGCCTCTCCGTGACTATAAGAAGGAGTCTCATCTCAACGGCATTCTCCACGGAG  
 CGTTTCTGGGAATCGGCATCAGGCTCTTCTTTCTCTGTGCTGGCCCTGATCATCATGAAG  
 ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGGCACAGCAC  
 GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
 AAGCCACACCAACAGTCTCTCGGACCCCTCTCCACCGAGTGCTCCCTCCCGAGATCAAG  
 AAGAACCACCAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCTCAAGC  
 CCCAGAAATCCAGGAGAGCCAAAGAGGAGTCCATTATGCCACGCTCAACTTCCAGGCGTCA  
 GACCCAGGCCCTGAGGCCCGGATGCCAAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTT  
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
 GTTGAAGATAACAGAGTGCAAAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCAGCCCTGTAATC  
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTTCAGACCCAGCCTG  
 GCCAACCTTGGTGAACACCCGCTCTCTACTAAAAATACAAAATTAAGTCTGGCCTGTTGGCAG  
 CGCCTGTAATCCTACTACTTGGGAAGCTGAGGCAGGAGATCACTTGAACCTGGGAGACGG  
 AGGTTGCGAGTGAAGCAAGATCACACCATTTGCAGCGCCAGCCTGGGCAACAAAGCGAGACTCCA  
 TCTCAAAAAAATAATCCTCAAAATGGGTTGGGTCTGTAAATCCAGCACTTTGGGAGGCTA  
 AGGTGGTGGATTGCTTGAGCCAGGAGTTCGAGACAGCAGCTGGGCAACATGGTGAACCCCT  
 ATCTCTACAAAAATACAAAAATAGACTGGGCTTGGTGGTGTGTGCTGTGAGTGTGCTGTG  
 CAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
 TACTGGGCTGCATTTCTCAGACAGTGGAGGCATTCTAAGTACAGAGTGAAGCAGGAGGTCG  
 TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAAGTAAAGAACCAACAAA  
 ATCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCTCACTGCTACACTCTCT  
 GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
 AAAGGGGAGGAATGAATAATCCACCCCTTGTGTGCAAAATGAAGCAAGAAATGAACATAAAA  
 GTGGGCAACAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATCTTTTGTCTCTT  
 TACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

0978192.101504

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLP L L L S S L L G G S Q A M D G R F W I R V Q E S V M V P E G L C I S V P C S F S Y P R Q D W T G S T P A Y G Y W F K  
A V T E T T K G A P V A T N H Q S R E V E M S T R G R F Q L T G D P A K G N C S L V I R D A Q M Q D E S Q Y F F R V E R G S  
Y V T Y N F M N D G F F L K V T V L S F T P R P Q D H N T D L T C H V D F S R K G V S A Q R T V R L R V A Y A P R D L V I S  
I S R D N T P A L E P Q P Q G N V P Y L E A Q K G Q F L R L L C A A D S Q P P A T L S W V L Q N R V L S S S H P W G P R P L  
G L E L P G V K A G D S G R Y T C R A E N R L G S Q Q R A L D L S V Q Y P P E N L R V M V S Q A N R T V L E N L G N G T S L  
P V L E G Q S L C L V C V T H S S P P A R L S W T Q R G Q V L S P S Q P S D P G V L E L P R V Q V E H E G E F T C H A R H P  
L G S Q H V S L S L S V H Y K K G L I S T A F S N G A F L G I G I T A L L F L C L A L I I M K I L P K R R T Q T E T P R P R  
F S R H S T I L D Y I N V V P T A G P L A Q K R N Q K A T P N S P R T P P P P G A P S P E S K K N Q K K Q Y Q L P S F F E P  
K S S T Q A P E S Q E S Q E L H Y A T L N F P G V R P R P E A R M P K G T Q A D Y A E V K F Q

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins  
signature.**

amino acids 365-371

0976193.101544

# FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGCTGTTATTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAACAAAGA  
AAGTCAAGCAGCCAGTGGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTTGA  
CAATGGAAACCAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTATCA  
TTGATGAAAGAAACAGGTGACATATATGCCATAAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTCTCAAGTTTCCGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
CGTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGGTG  
TCTGGAACCAACAGGTGTATTAATTTAACTTTTCAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAACCAATTTGACATTATTACTAATCATGAAACTCAAGAAGTAATAGTTATATTTAA  
AAGAAGAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCAATTAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTCCATATATGTAATTTGAAGTTTGTGA  
AGAAACCCACAGGGATCAATTTGAGGCGTGGTGTCTGCCACAGACCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATATGTATCAATC  
ACTACAAGTAACCTCAGTGGATCGTGAATCAGTGGCTGGTACAACTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAAACATCA  
ATGATCATGCTCCTGAGTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
TTACTTTTAACTCTATCTGTAGAAGACATAACAATTCAGTTTTCAAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTTGACTAATAGAACTGGTTTAAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTTGCCGACAATGGAATCCCGTCACTTACAAGTACAACACCCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTCCAGTACAGGAGCTTG  
TGCTTTCCATGGGATTCAGACAGAAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA  
TTTGGGTTTATTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGTA  
GAAAAGTGAAGATTTAGAGAGAAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAAACGCAAGACT  
CGGAAAACCAACAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTTGGCCCGCA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAAGCTCGAAGAAGCTAATATGATCCGTGTG  
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGGGGAAACAGGGTCAATAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATCTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTCTGTCAGTGCAGTCAAATAATTAGG  
GCTTTTACCATCAAAATTTTTAAAGTGCTAATGTGATTTGCAACCCCAATGGTAGTCTTAA  
AGAGTTTGTGCTCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAACTACCTACATGCTGTCAATGAACAGAGATGTG  
GGGAGAAATGTAAACCAATCAGCTCACAGGCATCAATACAACAGGATTTGAAGTAAATAAGT  
TAGGAAGATATTAAGAGTAGATGAGAGGACAAGAGTGTAGTGCATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAGAGTAAAAATACCAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTTTAT  
TTAAA

00703103-111771

## **FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906  
><subunit 1 of 1, 772 aa, 1 stop  
><MW: 87002, pI: 4.64, NX(S/T): 8  
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGVWVNQFFVPEEMNTTSHH  
IGQLRSDLNNGNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARL  
LYSLQQGQPYFVSVEPTTGVIIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD  
VNDNKPIFKESLYRLTVSESAPTGTSTIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TOEGIVILKKKVD FEHQNHGIRAKVKNNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYVFEVFEETPGQSFVGVSATDPDNRKSPIRYSITRSKVFNIINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYQVLNINDHAPEFSQYYETYVCENAGSGQVIQTI SAVD R  
DESBHHFYPNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTINTLTIHVDCDGSSTQTCTCYQLVLSMGFKTEVIIAILICIMIIFGFIFLTGLGKQ  
RRKQILFPKESDFRENI FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGLSLSLESAVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSN

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254



## FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTCGCAACATTGACATTATT

0978193.104501

# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGGCCCGGGCGCGGACCCCAACCCCGAC  
 CCAGAGCTTCTCCAGCGGCGGGCGCAGCGAGCAGGGCTCCCGCCTTAACCTTCCTCCGCGGGG  
 CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACTCTCCGCTTCTGCACCTGCCA  
 CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCAACGCGGGGCTGCACTGTTGGGC  
 TTCACTTCGCTTCTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCACTGGAG  
 GATTTACTCTTATCGCGGCACAACATCGTGACCGCCCAAGGCCATGTACGAGGGGCTGTGGA  
 TGTCTCGCTGTGCGAGAGCAGCGGCGAGATCCAGTGCAAAAGTCTTTGACTCCTTGTCTGAAT  
 CTGAGCAGACATTTGCAAGCAACCCGTCCTTGATGGTGGTGGCATCCTCTCTGGGAGTGAT  
 AGCAATCTTTGTGGCCACCCTTGGCATGAAGTGTATGAAGTGCTTGGAAAGCATGAGGTGC  
 AGAAGATGAGGATGGCTGTCTATGGGGGTGCGATATTTCTTCTTGCAGGCTCTGGCTATTTTA  
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCATGACCCATGACCCCACT  
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
 TTCTGGGAGGTGCCCTACTTTGTCTTCTGTCCCCGAAAAACAACCTCTTACCAACACCA  
 AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAGACTACGCTGTGACACAGAGGCAAAAG  
 GAGAAATCATGTTGAAACAAACCGAAAATGGACATGTAGATACATATTAAACATTAGGAC  
 CTTAGAAATTTGGGTATTGTAATCTGAAGTATGGTATTACAAACAAACAAACAAACAA  
 ACCATGTGTTAAAAATCTCAGTCTAAACATGGCTTAATCTTATTTTATCTCTTCTCTCA  
 ATATAGGAGGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATGTAGATTAATCACTCAAA  
 GGGGGAAGGGGTGCTCTCTTAAATATATATAGATATGATATACATGTTTCTTATTA  
 ATAGACAGTAAATACTATTCTCATTATGTTGATAGTATAGTAAATATCTCTAAAT  
 AGGTAAATGTATTAAATCCATATTGATGAAGATGTTTATGGTATATTTCTTTTCTGCTC  
 TTATATACATATGTAACAGTCAAAATATCATTTACTCTTCTTATTAGCTTTGGGTGCCCTTG  
 CCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATCTCTCATGCGTGCCTTTT  
 CATATACCTATTTTTATTTTTTACCATAATCTTATAGCACTGTCATCGTTATTAAGCCCTTAT  
 TTGTTTTGTGTTTCATTGGTCTCTATCTCTCTGAATCTAACACATTTTCATAGCCTACATTTA  
 GTTTCTAAAGCCAAAGAAATTTATTACAAATCAGAACCTTTGGAGGCAAAATCTTCTGCAATG  
 ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTAATCTGACCCATAGCACT  
 CTTGTTTGTCTTTGAAAATATTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTGT  
 AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTCTATAGTTTTATATCCCCCTAACT  
 ACTTTTTTTTCCCCATTCCTTAATGTATTGTTTTCCCAAGTGTAATTTATCATGCGTTTTA  
 TATCTTCTTAATAAGGTGTGGTCTGTTTGTCTGAAACAAAGTGCTAGACTTTCTGGAGTGATA  
 ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTTCACTCTTTT  
 TTCTATCTGCCAAATTGAGATAATGATACTTAACCAAGTTAGAAGAGGTAGTGTAATATTAA  
 TTAGTTTATATTACTCTTATTCTTTGAACATGAACCTATGCCTATGTAGTGCTTTTATTGCT  
 CAGCTGGCTGAGACACTGAAGAAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATT  
 CACTGCTTCTCTCTCTACCACTTATTTCCTGAAACAAACCTACACATACCTTCACT  
 GTGGTTCAGTGCTTCTCTCTTACCAGTCTATTTCCTGAAACAAACCTACGCACTCAT  
 CTTATGTGGCTCAGTGCTTCTCTCTTACCAGTCTATTTCATTCTTTTCACTGTGCT  
 GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG  
 CTATTTCACTTGAGCAAGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
 GATTGAGTCTTGGTGTCTCAATCACCGTCTGTGTTTGAAGCAAGGCATTTGGCTGTGTAA  
 GCTTATTGCTTCTCTGTAAGCGGTGGTGTGTAATTCCTGATCTTCCCACTCAAGTATG  
 TTGTGGGATCCAGTGAGATAGAATACATGTAAGTGTGTTTGTAAATTTAAAGTGTCTAT  
 ACTAAGGGAAGAAATTGAGGAATTAAGTGCATACGTTTGGTGTGCTTTTCAAATGTTTGA  
 AAATAAAAAAATGTTAAG

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAFGLWGIAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVQSSTGQI  
QCKVFDLSLLNLSSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATANYGNRIVQEFYDPMPVPVNARYEFGQALFTGWAAASLCLLGGALLCCSC  
PRKTTSYPTPRFPYKPPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGGTGTTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAA  
CNTTCAACANTTCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCCTGTCCC

0078103-101501

## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCITTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

0976193-201501

## FIGURE 101

GGGCCCGACCATTTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGGATATTTCTT  
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

097013-10104

## FIGURE 102

ATTCTCCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTGCGAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCCTATGACCCCGATCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTCTGTC

0978193.101544

10503-10504

AGAGCACCCGGCAGATCCAGTNCAAAGTCTTTGACCCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGGAAGACGATGAGGTGCGAAGATGAGGAT  
GGCTGTCA TTGGGGCGCGATATTCTTCTTG CAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNNTTCNGNNGNTTCATGACCCCTATGACCCAGTCAATGCCAGGTAC  
GAATTGTGCTCAGGCTCTCTTCCATCGCTGGGCTGGGCTGCTCTCTCTGCTTCTGGGAGGTGC  
CCTACTTTTGCTGCTCTGTCCTCCCGAA



## **FIGURE 104**

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTT  
CTTNTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTTCTGCCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTTCCGCAACC

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## FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATINTATGACCCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTGCTGTTTCCTG

09978193.101501

## FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTG  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCCCTGTCCCCGAAAAACAACCTCTTACCCACG

0978493-104501

## FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNATGTCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTTCTTCTTG  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCATGACCCCACTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCAGAA

0076193:104664

## FIGURE 108

GCGTGCCGCTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCGCTGCCCCG  
ACCGGTCCCCGCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGTGCTCCGCCGTAAAGGAACATGGCGAAGGTGGAG  
CAGGTCTGAGCCTCGAGCCGACGACGAGCTCAAATTCGAGGTCCCTTCACCGATGTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAAGTAAACAAGTT  
TATGGTTCAGTCTATGTTTGTCTCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAG  
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACCATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGACAGAGCAACAGCCCCATTTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTCTTTA  
TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACAAAAATATAATGTAACGATCTTTTAGAAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCCTTCTCGCCTGTGGTGTGGCCCTTGGGGAGCTGGAGCCCGCAT  
GCTGGGGAGTGCGGTGAGCTCCACAGTAGTCCCAACGTGGCCCACTCCCGGCCAGGCTG  
CTTCCGTGCTTCAGTCTGTGCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGATTTGGTTCACTGATGAGTGAAGTCAAACTGTTATTAGAGATGTTTAAATGCATA  
TTTAACTTATTTAATGTATTTTATCTCATGTGTTTTCTTATTGTCAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACCTGTTGGGTGAACGTGTTATTGCTGCTGGAGGCTGTGGGCTCCTGT  
GTCTCTGGAGAGTCTGGTCACTGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCTGGAGTCAGGACAAATGGATCGGGCTCGAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGGAAGAGAGAACTCTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGAAGTGAATTTTATGCCATAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAGAAAAATTATAATAAGCCCCAAAATTAGAAAA

09978493.101504

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977  
<subunit 1 of 1, 243 aa, 1 stop  
<MW: 27228, pI: 7.43, NX(S/T): 2  
MAKVEQVLSLEPQHELKFRGPFITDVVITNLKLGNPIDRNVCFKVKTIAPRRYCVRPNSGIID  
AGASINVSVMQLQPFYDYPNEKSKHKFMVQSMFAPITDTSDEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIISTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIKIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

0076193-104604

## FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTGGGTGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAAGAAATCTTTTGTCAATTTGTACATTTGCTCTATGGGGGAATTATTATTTT  
ATCATTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAAATGAGC

0070193.01501

## **FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT  
CCGTGTCCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

0978193.103501



## **FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNCGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

0978193-101504

## **FIGURE 113**

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCGGTNTTCAGTTCGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCITTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

0978193.101501

## **FIGURE 114**

TGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCAACAAGAGTACAGTTAA  
TGCTGCGTGC

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## **FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTTGTAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTTGANTGATTGACCCAGCGCTTGGAAATAAATGGCAGTGCTTTGTTCANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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## **FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTTCGGTGCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACCTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

## FIGURE 117

GCAGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGCAGTGGCC  
CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAATAATGCTGCTTTGGTTGATATTTTTACC  
CCTGGGTGGACCTCATTTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTTGTCAGTGAAGGACTTTCATCTCACCAGCCCCGCATTGTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAATATCACCACAAGGGGAG  
TATCTGTTAGGAGAAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAAGCATCTTGGACAAA  
AGGTTCTTAACCAATTTCCCTTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCCTCAGCATGTTCTAAGTGTGCTGCCACTGTGTTTATGATGGAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAGAGAGGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGCTC  
AGAGGATTGCCGAAGGGAGGCCCTTCTTTTCAAGTGGACCCGGGTCAAGAATACCCACATTCG  
AAGGCTGGGCAAGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGTCTCAAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
TGCTGGTGGAAATGATCCAATTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATAGTCGGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCCTAAATACGCCAGATTGCGCTCTGGAATCACGG  
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGATCATCTAA  
TCACAGAGAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCGGACTT  
GAACCTGTCAATAGCATTTCAACATTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
CATGTTGATGAGTTTCAATTTGTAGAAAAATTTTGTGTCCTTCTTAAAAATAGACACACTTT  
AAACCTTCAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCAAGCTCATGCCCTCAATGTTTATATTGTGTTTATCTGTTGGGTCT  
GGGACATTTAGTTTATTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTTATAAA  
CAAACTAATAACTGTTTATCTGCTTTTGAAGAAATAACAATTACAATGTGTATTATTATTAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAAATTGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGTGCTACATTTTATAGGACAAGAAATCTGTAATCTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGTTGAATTTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCTTAAATGAATAAAATTTATGAATATGA

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## FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSLELDYLSYETVFENGTRTLTRVKVQDLVLEPTQNIITTKGVSRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISQPHVLTAACHVHDGKDYVKSGSKLRV  
GLLKMNRKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

0078193.101504

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCGGAITCTGATTCGGCAAGG  
ATCCAAGCATGGATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCTGAGTTCACGAGCCGACGCTCCGAGGAGGACCGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCAGCACCTGCGGGGGAGGGGCCCTCTACTCTCTGAGGCGCT  
GCCGTAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAACTTTTGGATATGTGCATCAGTGGTTTATGCCAAATTTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGCTGCGAACGGAGATGGGTCCA  
CTGCGCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT  
GTGGTTGCATCTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTCTGATCACTT  
ATATCTGGAAACCAAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTTATTGTCAAGATTTCGTAACCTCGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCTTCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGTCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCAAAAAACAAAGCCCAATATAAAGAGGAATGCATCGTACCCACTCCTGTCTATA  
AACCCAAAGAGAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGAGGAGCCCTCGTTAAGTGTGTAAGGACACAGACTGTTCTATA  
TTTGAAACTGTTTGTGTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTGGCTCTCAAATTAAGATTGATTGTTTCAA  
AAAAAAA

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## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDANGPWSSECSRTC GGGASYS LRRLCS  
SKSCBGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNP CSLKCQ  
AKGTTLVVELAFKVLVDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDPHLYLETKT LQGTKGENSL SSTGTFL  
VDNSSVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP CS  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP CPASDGYQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKL PVEAKLPWFKQAQEELEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

0570103-104504

## **FIGURE 121**

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCGCCGGTTCTGTGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGTGATCACCGGGGCSAACAGCGGCCCTGGGCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGTGATCATGGGTGCGGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGTCTCCGCCGCGAGCTCCGCCAGGCGCGGAGTGTGGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTCGCTCGTGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTGTCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACATTCCTACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCAGACTTCCATTATT  
GGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTACTGAAAAATTATTTT  
TGGGATAAGAGAAATTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAATTAATCTGC  
CTGGTGTGTGCACAAAGTCTTACTTGAATAAAATTTACTGTTAC

0978493.104504

## **FIGURE 122**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLGLLKSSAPSR  
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRELEGTNTVTNVLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

0123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

## FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAATTATCTGCCTGGCTT

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## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGGCTCCCGAGCCAGCC  
CTTTCCTAACCCAAACCACTAGCCAGTCCAGCCGCCAGCGCCTGTCCCTGTACGGAC  
CCCAGCGTTACCATGATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAGCTTCCGATGTCATTAAAGGAAGAATT  
TCCAAATGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTTGGCAGATTACATCAGGCAACAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACCTTGATCGCAGCAAAAGAA  
ATATCAATTGGATATTTTGGAGAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACGAGGCATTCCTCGGATATGTTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAGGTTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTG  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG  
AAAAACAGTTTGTGAAGCCTTTCAACAGCAGCATCAACCTACGTTGGTGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGATTTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 125**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVIWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCFVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
```

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

## FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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# 1. Introduction

AGAGGCCCTCTCTGGAAGTTGTGCCGGGTGTTGCCCGCNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGCGCTCCCGAGCCAGCCCTTTCTTAACCC  
AACCCAACTAGCCCGTCCAGCGCCAGCGCTGTCCCTGTCTCNGGANCCAGCGTNACC  
ATGCATCCTGCCGCTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGGTGTGCTTTCAGTCAG  
ATGTGGCATCCAAATTTTGTAGGANGCTTCCGATGTCATTAAAGGAAGAATTTCCAAATGAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGCATAGCCCAGAGATACAGGA  
TAAGCAATAACCCAACTCAAAATGTTTTCGTAAATGGGATGATGTAAGAGAGAATAACAGG  
GGTCAGCGATCAGTGAAGCATGGCAGTTTATCATCAGGC



## **FIGURE 128**

GCCCA CGCGTCCG **ATG** GCGTT CACGTT CGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCTGAATCCCCTTGTA CTCTCCAGAGTACCTCAT  
CCAGCGTTTCTTCTGTGTGTCATGTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA  
CTCTATGACCC TACAACCATCATGAATGCAGATATCTAGCATATTTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCT **TAGA** CAACAACACAGAAAGAAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGCCTTGGAAGACTG  
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAACCTGCAC TTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCC TAGTACATTGGAAGCTTTTGT TTATAGGAAC TTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAAC TGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

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**6033**



&lt;MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIIHAFF  
CVMFLCAAEWLTGLGNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYLYGMIYVLVSS

Signal peptide:

amino acids 1-20

## amino acids 11-31

amino acids 57-77 and 123-143

amino acids 57-77 and 123-143

# FIGURE 130

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCCCTG  
AATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTITT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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## FIGURE 131

CGGACGCGTGGGGGAAACCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC  
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTCAATTGTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAAATGTGAATCTGCATGTACA  
GAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTGGTTGCCAGAATCAGCTGCC  
ATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCACTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTAAAGATGCCCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGAGTTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAATTCCTCTCATAGAGCTTTTAAATGGTTTCA  
TTGGATATAGGCCTTAAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG

## FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECE SACTEAYSQSD EQYACHLGCCQNQLPFA  
ELRQEQLMSLMPKMHL LFP LTLVRSFWS DMMSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

0076193-14604

### **FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCCG  
TGAAC TGAGACAAGAACAAC TTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

0978193-164504

## **FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTCGGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTGTGAGTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCTCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

0070491366004

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGGCCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTAAATAACTACAGGCCTTTCCCAAGACTACAAAA  
ACTTCTTGAAGTGACTACTTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTCAAGTCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCACTACGAAGAAAACCTGTTTAAAGCCAC  
AGACAATTAAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTGAGTGCAGATATCTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTGTATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAATACTTCATGAAATCAAGTCATTTCTTTG  
CATTTTGATGAGAATTCATTTTGTCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAAATATTCAAGAAATATGGATTGTGTTGGTTGTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTAAGAAGATTAGAAAAC  
TCAGGAACCTGTTACAGAATATTCAATTAAGAAAAACAAGCTGATATGTGCTGTTTCTGAC  
AATGGAGGCGAAAGAGTGGAAATTTCAATCAAAGGCATAATAGCAATGACAGCTCTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTAAAGTAAACACATTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAAATATTGAATAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

007073-10504



## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDLDDCTCDVETIDRFNNYRLF  
PRLQKLLSDYFRYYKVNLRKPCPFWNDISQCGRRDCAVKPCQSDVEPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLNPE  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRLKNLYFLYLI  
ELRALSKVLPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGSPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

[illegible]

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAGATATCTTTTACAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACCTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCACAGATTTTCAACTNNTTACTGGAATAAAATTCCAGGATGAGGNAAACAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCTACTTTTGATGAGAATTCA  
TTTTTTTGGCTG



993101

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
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><subunit 1 of 1, 124 aa, 1 stop
```

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPPNLDDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

### Important features:

**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

## Integrins alpha chain proteins

amino acids 67-81

## **FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAATCCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCTCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATACCCACGCCT  
ATTCACAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAAC TGGGAAATT CATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

0076193.101501

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCACTTCGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA  
**AATG**CAGACTTTCACAAATGGTTCAGAAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTCT  
ACGCATTGATTCATGTTTGGTCCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAAGTGATCGCGCCTGGAGA  
AACAGTGTAATACTCTGTGCAATACCAAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATAACCTTCGTGTGAGGGCCACATTGGGCTCAGAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAAATGTCAAATGGTGAGGAGTGG  
GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGGCTTTGTTGGCTTCATGCTGATCTCTTGT  
GGTCTGTCGCACCTGTCCTGGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
TGGTCTCTCCAGACACCTTGAAAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCAGGGCCCTGGAT  
CTC**ATAG**TTTTCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC  
ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACGAGAAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCAAGCCACACTGAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCCAGCAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAA

0978193.101501

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFMTVLBEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPEE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQTSAN  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRRPEGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVVEVQGEAIPVLVLAFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

## **FIGURE 143**

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAAC TGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCTTGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCAGGGCCACTGTGCCATACAACCTTTGTGT CAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCCTTGTCGCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

097543-14304



## FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGTTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTCTGTGGGGAAGCGGCAGAGCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCGCTGACCCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAACCTGCGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACAGGAACTCTACGGGAATTTACGCGCTGCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC  
CAGTCGCCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGACCCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAAACAGCCGGCCCTGCGAGCCTTGGCCCAAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCATGGTGCCTGAGACTCCCTTCGAGGATTGCACCGCCCGTCTTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

007643.104504

## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLVDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLNDRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWWILIDRALNITSLQMHSLRLLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 177-199

**N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

0076193-101504

# FIGURE 146

GGCGCCTGGTCTCTGCGGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGACGCTCCGCCCGAGCCTC  
 GTTCGTGTCGCCGCCCTCGCTCTCGCAGCTACTGCTCAGAAACGCTGGGGGCCACCCTGGCAGACTAACGAA  
 GCAGCTGCCCTCCACCCCAACTCGCAGGTCTAATTTTGGAGCCTTTGCGCTGCCATTCTTCCAGGTTGAGGGAGC  
 CGCAGAGGCGGAGGCTCGGATTTCTGTCAGTCAGCACCACCGCTCGCCCCCGAGCCGCTCGGTGTCTCAGGCCCTTC  
 GCGAGCGGGGCTCTCGCTCTCGGCTCCCTTTGAAAGGCTCTGGGCGGCTCGCAGAGCGCGGCGCTCGGTTTGGGT  
 CACCTCTCCACGGAACCTTACACATGGAGAGCCAAAGGAGTGGAAAGGCTGTCTTGGAGATTTCCTTGGGGA  
 ATCTCTAGGTCTATTCAATTGAGGTGTACCGCGCGGGAGTGGCTCAGAGTAACCCACAGTGTCTTATGGCTAGA  
 GCAATTCCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
 GAGTGGTGATAGCCAAACCAAGGGGAAAGGGCCATCACAGACAATGACATGCGAGATTTTTGGACCTTCAT  
 AATAAATTACGAATCAGGTGTATCCACAGCCTCTAATATGGAGTATATGACATGGATGTAGAGCTGGAAAGA  
 TCTGCAAGATTCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTGGAGATTTCCTTGGCAAGAT  
 TTGGGAGCACACTGGGGAAGATATAGGCCCGCAGCTTTCATGTACAATCGTGGTATGATGAAGTGAAGAGCTTT  
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTGAGGTGTTCTGGCCCTGTATGTACACATTATACA  
 CAGGTGCTGTGGGCACTAGTAAACAGAAATCGTTTGGCCATTAAATTTTGTGCTAACAATGAACATCTGGGGGCG  
 ATATGGCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCAAGGGGAACTGGTGGGGCCATGCCCTTTACAA  
 CATGGGCGGCCCTGTCTGCTTGGCCACTAGTTTGGAGGGGGCTGTAGAGAAAAATCTGTGCTACAAAGAGGG  
 TCAGACAGGTATTATCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC  
 CATGTCGGCACAAGATCAGATGATAGTAGCAGAAATGAAGTCAAGCGCACAGCAAAATGTCCCAAAATGTTTCT  
 TGTGAAGTAAAGATTGAAGATCAGTGCAAGGAAACAACTGCAATAGGTACGAATGCTGCTGGCTGTTTGGAT  
 AGTAAAGCTAAAGATTATGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTATTATGGT  
 ATAATAGACATGATGTGGCTGTGGGTAGATATCACTAGACAGGAAGAAAGCATTTTCATCAAGTCCAATAGA  
 AATGGTATTCAAACAAATTTGGCAAAATCAGTCTGCTAATTCCTTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG  
 ACTTGTGAAACAACTGTGGAAACAGCTCTGCTCAATTTCTAAAGCTGCTTCAATTTGCCCAAGAGTATCTGCTCT  
 CGTAACCTGTATCAGCAAGAAATCCACATTTATGCTCGGTGTAATTTGAACTCGAGTTTATCTGATCTGTCCAGTATC  
 TGCAGACGACGATACATGCTGGAGTGTGCGAAATCAGGTGGTTATGTTGATGTAATGCTGTGGACAAAGA  
 AAGACCTACATTGCTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAAATCTTCCAGGAGGAAAGGCATC  
 AGAGTGTGTTGCTGTTGTGTAACATGAACTCTGGAAGAGGACATAAAGACTTTCCAAATGCAATATTCTGA  
 ATTTTGTATAAAACGTGAACATTACTGTACAGAGTACATCAACTTTTCAGCCCCAAAAGGTGCCAAATGTCATA  
 TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGCGAAAAGTAATGAATAATAATGG  
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTCTAGCAGTATTCTTACAGTTAATACATAGTCATGATT  
 GTTCTACGTTTCATATATATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGATGTGAATG  
 GCCCTCAGAAAAATCATCTAGTGCATTATAAAATAATCGACTTAAACCTGAAAGAAACCTTATCACATTTTCCC  
 AGTTCAATGCTATGCCATTACCAACTCCAAATATCTCAAAATATTTCCTACTTAATACTGTAAAGTTTCTTC  
 TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATATATCCCTTAATATC  
 CAAATGAATCTGTTAAATGTTTGAATCTTGGGAATGGCTTAAAAATAAATGTAATAAGTCAGAGTGGTGGT  
 ATGAAAAATTCTCTAGTGATCATGTAGTAAATGTAGGTTAAGCATGGACAGCCAGAGCTTCTATGTCTGTTA  
 AAATGAGGTACATATTTCTTTGTATCTCGCAAAATCTCTCGCAGGCCAGGAGTATAATAGCAAAAGGT  
 GAACAAAGATGAATTAATGTAATTAATTAACATTGCACTGATTTTTAAATGGTAAATGACCTTGTATATAA  
 ATATTGCCATATCATGTAGTACCTAATATGGTATATATTTGTTCTATGAAAAATGTATGTGCTTTGATATCAA  
 AATCTGTAAAAATGTAGTTTGTGAATTTTTTCTGCTGGTGGATTACATATAAATTTTCTGCTGGTGGGA  
 TAAACATTAAAAATTAATCATGTTTCAAAAAA

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLKLYMDEEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPA SLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC  
HNMNIWQIWPKA VYLCNYSYPKGNWWGHAPYKHGRPC SACPSPFSGGCRENL CYKEGSDRY  
YPPREETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR  
YEC PAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI  
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCFPHKPASHCPRVYCP RNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31

## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCGCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCTCCCTGCTCCCACGCCG  
CGCCCCCTCCGGTCAAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAAGGAGCACTGCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAACCAAGTTGGGAGACTTGTGCAAAGGA  
CTTTCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGCTTTCCCTTTTAA  
AAAATGCTTTTGTATTGTCCATACGTCACATATACATCTGAGCTTTATAAGCGCCGGGA  
GGAACAATGAGCTTGGTGGACACATTTTCATGCAGTGTTGCTCCATTCTAGCTTGGGAAGC  
TTCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCGTAGCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACCTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTACACACCTTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGCTCTTTCCAACCTGAGGATTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCTCTTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCTCTGTACATATACCCCTTAAGAACGCCCCCTCCACACACTGCCCC  
CAGTATATGCCCATGTGACTGCTGTGTTATATGCTATGTACATGTGAGAAACATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAGTAATAAAATATATTGAAATGTAAAA  
AAAAAAAAAA

0978193.301501

## FIGURE 149

MSLLPRRAPFVSMRLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNANWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

00070193.101501

# FIGURE 150

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCCTGGTCATGTTAAACTCCAATGTCCTCTGTG  
 GTTAACTGCTCTTGGCCATCAAGTTTCACCCCTCATTGACAGCCAAAGCAGATATCCAGTTGTCAACACAAATATGG  
 CAAAATCGGGGCTTAAGAACACCGTTACCCAAATGAGATCTTGGGTCCAGTCGGAGCAGTACTAGGGCTCCCTTA  
 TGCTCACCCCCCATCGGAAGAGCGGGTTTCAGCCCCAGAACCCCCGCTCTCTCGGATCGCATCGGAATAC  
 TACTCATTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGTCATGACATGCTGCCCATCTGGTT  
 TACCGCAATTTGGATATCTTTGATGACCTTATGTTCAAGATCAAAATGAAGACTGCTCTTACTTTAAACATCTACGT  
 GCCCAGGAAGATGGAGCCAAACAAGAAAGAACGCGAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
 TATTCTATGATCAGAACGTAAGAAGCCCGTCATGCTATATCCATGGGGGATCTTATCATGGAGGGCACCAGCAA  
 CATGATTGACGGCAGCTTTGGCAAAGCTACGGAACCGTCACTGGATCAACATTAACCTGTCGGAACTCTGGGT  
 AGGGTTTTTAAGTACCGGTGACCAAGCAGCAAAAGGCCAATATGGGCTCCTGGATCAGATTACAGCAGCTCGGGT  
 GATTGAGGAGAAATGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
 CTGTGTCAGCTGTTGACCCCTGTCCCACTACTCAGAAGGCTCTCTCCAGAAGGCCATCATTACAGAGCGGCACGCG  
 CCTGTCCAGCTGGGCGAGTGAACCTACAGCCGCGCCAAAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACAT  
 GCTGGACACCCAGGACATGGTGAATGCCCTGGGAAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCAACCC  
 GGCACCTACCAATAGCCTTCGGGCCGGTGATCGACGGCGACGTCATCCAGACGACCCCGAGATCCTGATGGA  
 GCAAGCGGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAGGGGAAGGCCGAAAGTTCTGGAGCGGCAT  
 CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
 CTACCTTCAGGGGAAGACATTTGCGGGAGACTATCAAGTTCTATGTACACAGACTGGGCCGATAAGGAAAAACC  
 GGAGACGGGGGAAAAACCTGTGGCTCTCTTTACTGACCCAGTGGGTGGCCCCCGCGTGGCGCGCCAGCT  
 GCACGCGCAGTACGGCTCTCCCACTACTTCTATGCTTCTATCATCACTGCCAAGAGGAAATGAAGCCGAGCTG  
 GGACAGTTCCGCCCTACCTGGTGATGAGGTGCCCTATGCTTCCGGCATCCCATGATCGGCTCCACCGAGCTCTTCA  
 TTGTAACCTTTTCAAGAACGACGCTCATGCTCAGCGCGGTGGTCATGACCTATCTGACGAACTCTCGCAAACTGG  
 TGATCCAATACACCGATTCTCAGGATACCAAGTTCTATTACACAAACCCCAACCGCTTTGAAGAAGTGGCTCTG  
 GTCCAAATATAATCCCAAGACAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCTACTACGGGC  
 AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCTCATTTGCAACCTTGAACTGAAAGATATTCAGTATTGTTCAAC  
 AACCAACAAGGTTCTCCACCGACATGACATATTTCCCTATGGCACCGGGGATCTCCCGCCAGATATGGCC  
 AACCAACAAACGCGCCAGCATCTCTCTGCAACAACTCCCAACACTCTAAGAGACCTTCAACAAACCGGGCTGA  
 GGACACAACTCTCTCATTTGAACCAAAAGGAGATTATCCACGAAATTAAGTGTCAACATTGGCCGCGGGCGTC  
 GCTCTCTTCTCTCAACATCTTAGCTTTTGGCGGCGCTGACTACAAAAGGACAAAGAGGCCATGATGATCTCTGACAT  
 CTACACCTCTCAGCTCGCGCGGTGGCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAA  
 CACATGACGGGGATGACGCTTTTGACACTTTTAAACACCTTCAGTGGGAGCAAAACAGTACAAATTTACCCCA  
 CGGACATTTCCACCACTAGAGTATAGCTTTGCCCTATTTCCTTCTATCTCCCTACCGCTACCCGCTCAGCAACAT  
 AGAAGAGGGAAGGAAGAGAGAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCGGAATGTTTTTGTCCCACT  
 GACTTAAGACAAAAATGCAAAAGGCGAGTCATCCATCCCGCAGACCCCTTACGCTGGTGTCTTTCCAGTATTAC  
 AAGATCAACTCTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAAATACTGCTTTAAGATCTCTTACCA  
 CTCCAATCAATGTTTATGTGTATAGGACATCACATTTCAAGGCCCGGGTGTCTTCAACGTCATGGAAGCAGCT  
 GACACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC  
 CACACAAATGGATGCTCTCTTTAAGTGAAGAAAGAGTCAATGAGATTTTCCCGCAGCATGGAGCTGTAATCCAG  
 AGAGAAGGAACGTAAGAAATTTATTTATAAAGAAATGACTGTGACGCGAAATCTGTACGGTCTGTGCAAGAG  
 GTGTTTTGCCGCTGAACATTTTAAAGAGACTTTGT

0976193.101501

## FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLENEILGPVEQYLGVPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLEIWFATANLDTLMTYVQDQN  
EDCLYLNIIYVPTEDGANTYKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQIILMEQGEFLNYDIMLG  
NQGEGLKFVDGIVDNEDGVTNPNDDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPPYV  
FGIPMIGTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTE LSVTTI AVG  
ASLLFLNILAFAALYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDECE  
SLQAHDTLRLTCPDYYTLTLRRSPDDIPLMTENTITIMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

0573437-16504



## FIGURE 152

GGGAAAGATGCGCGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAACCGGGAGCACTCGCTGTGCAAGCC  
CTACCAGGGTGTGGGCACAGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCTCGAGAGACTGGGAGTTGCAGGTGCACCTTCAAAATCCATGGACAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCTTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCTACAGAGCTGGGAGGCTGCACAGCCATTTGTCC  
GCAATCTTCATTACGACACCTTCCTGGTGATTGCTACGTCAGGAGGCAATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCCTGCC  
CCGCGGCTACTACTTCCGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCTTGAAGTTGTTTGAACGTGACAGTGGAGAGAACCCAGAGAGGAAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCTTGGCCCTTCTCCTCATCGTCTTTTCTCCTGGTGTCTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG  
GCCTGAGCATGCGACCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTGGGGACTATATTCTG  
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTGCTGTGATGGGGACATCTAATCT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCCTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAAATTCATAGCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTGT  
AATCCACAAGAATTAATAACTGGTAAACACCAAGGCTTCTGACCATCCATTGCTGGGTT  
TTGCAATTTGACCCCAACCCTCTGCCTACCTGAGGAGCTTCTTTTGGAAACAGGATGGAACT  
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGCTTCA  
TGGCCTTCATTAGGTGGCCCTAGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTTCAGGCCCTCAGT  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTACCAAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCTATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT  
TACGATTTTGGAAATCCCACTTTGAGTGCTGAAAGTGTAAAGGAAGCTTCTTCTTACACCTT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTCTTCTTAATGGACAAGAGACAGT  
TGCTGTCTCATGTTTCCAAGTCTGAGAGCAACAGACCTCATCACTGTGCTGCTGGAAGAGT  
CACTGTCAATTGAGCAGCAGCCCTGAGTGTGGCCTCTGTCAACCTTATTTCACTGCCCTTA  
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCTTGGAACTCTGAGTCCCTCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCAGATGGAACCAAAAAAAAAAAAAAAAAAGGCGCGCGACTCTAGAGTCG  
ACCTGCAGTAGGATAACAGGTAATAAGCTTGGCCGCCATGG

09978193-101501

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTQDMQSKQGGALWNRVPCFLRDWELQVHFKEHGQGGKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFGVGLGVFVDYTPNEEKQQQERVFPYISAMVNNGSLSY  
DHERDGRPTELGGCTAIVRNLYHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPMTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

0978703-101501

# FIGURE 154

CCGAGCCGGGCGCGCAGCGAGCTGGGGCCGGCTGGGACCATTGGGCGTGAGTGCAATCTACGGATCAGTCT  
 CTGATGGTGGGTCGTTAACTCAGTGGGGACTCCAAGATTTCATGAAGAAATCAGTTGTCTTCATTCAAGAAT  
 TGGGGTCTGGGTCGAATTCCTGCAGCTGGTGAATCTGTTTTCTAGAACGGTTTAATTAATGGCTCGAGTCT  
 GACATGTTCCCGATTTCAGGTGAACCATGAAGAGAAATAGATACTTAATAATGCTTTTCCGAAACGCTCTCT  
 TGCTGCTGCTGGGCTGGCTGGGCTGCTGGGCTTTGTAGCCTCAGCGTCAGTCTCTCCACCTGATCCCGGTGT  
 CGACTCTAAGAATGGAATGAGTAGCAAGAGTCAAGAGAAATCATGCCGAGCCCTGTGACGGAGCCCGCTGTGA  
 CAGACCCCGCTTTATGAAGCTCTTTGTACTGCAACATCCCGAGTGTGGCCGAGCGCAGCATGGAAAGGTCAIGCC  
 CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTTCATCCCA  
 AAACAAAGCGACAGAAATTTGACTGCACCTCTGGTGGCTAACAGGAAACCGTATACCCCAAACCTGGAAGCTTTTCA  
 TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTCGAAAGCCCGCTTGAATCTCTGCTCTTTACCCAAATCACC  
 CATTTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGACGCAATTTGCAGAACGGTCAGCTGCTGAGGGA  
 TCTATCTAAGAAACACAAACTCCTGCCCAATGATTTGCTCTGACAGACGCTCTATTAGAGACCACTGGGAAAA  
 GCCGGACCTCACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTC  
 GGCCACGACCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGTAAGAAACAGATATCTGGAAGAGGAGC  
 AGCTGCTCAGTACCTCTCTACGTTTGAAGAACAGCCAGCTGGAGAGACCTACGGGGAGATGGCCAAAGATCTGTG  
 ATGTCGCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTCTGCCCAATGTCACT  
 TTCCTGTACCCAGAAATGGCTGTGTGAATGGAGCACTTCAAGGTAAATTAAGACCCATCAGATCGAGGATGAAA  
 GGGAAAGACGGGAGAAGAAATTTGACTTCGGGTATTCTCTCGGGTGCCACCCCATCTGAACCAACCATCG  
 GCCGGATGCGAGGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACCTGT  
 CACCAAGTTCTCAGTGCCTTGGGCTTTTCAAGCCAGGTTCCCAAGGTTTGACGCGAGGTTGATCTTTGAGCTTT  
 GGCAGAAGACAGAAAGCCCAAGTGAACATTCGGTCCGGATTCTTTACAAATGGGCTGATGTCACATTCCACACT  
 CTTTCTGCCAAGACCAACCAAGCGCTTCTCCCAAGCCCATGTGCCCGCTTGAAACATTTGGTCCGCTTTGTGAAGA  
 GGGACAGTTCTTAGCCCTGGGTGGCAGTGGTACAAATTTATGATGATGTCACAGGGAGGATTCTAAAGG  
 TATGCACTACAGCAATATAGAATTCATGCCAATACAGAGCATAGGAAAGGTTCCACTGTAGTTTGTCTGATAC  
 TAAGGGTAGAAGATTATGCTTTTAAAGGCTAAATATTCTTTGTGGAAACCAAGATGTTGGGTTGAACAGT  
 AAGCAATTTGTCGAATGTGTACGTGAATGCTTGGTACAAATGGCCAGTTCACAGAGGAATGAAGGTAATCT  
 TATCATAGCCAGACTCTGCTTGAATGCCAGAAATATATAGTTCAAGACCTGAAATTTGCCAATGCCAATTTGCAC  
 TCTTCTGGCTGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCAAAAAATAGGCTTAATCTACAAATTC  
 TTTACCTTGTCTGTTGAAGAAATTTCTGAAGTGAATTTATCTAAATTAAGGTTGGCAACTTTCTCTGACAACT  
 GCCAGATTGTAAATATTTTCACTGCTGTGGACCAAAAGGCCACATACAGTCTGTGCATAACTCATCACTCTGT  
 TTCTGAAGCAGGAAGCCACACAGACAGTACATAAAGGAATATGTGAGCTGGGTTCCGAGGCGACAGCAAAACA  
 GATGGTGACCAAGACTTGGCCCTCGGGCTGTAGTTTGTGACCCCTCATCAAAAAATAGGCTTAATCTACAAATTC  
 ACTTCCAGCACTTTGAGAACAGGTTGAATACCAAGAATTTATCAATGGTTCCTCCAGTAATCTCTGCTAGAAACA  
 CAGAATTTGGTCTGTATCTGACACTAGAAACAAACTTGGGGTAAATAAACAATTGAATTAGAATGAATACATGAA  
 AACTGATTAGAAGAATCTTGATGTTTATGATGATTGTGGTCAAGATAGTTTAAAGTATGTTCTAAATATTGT  
 CTGCTGTAGTCTAATTTGCTGTATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTAGGAAAATATT  
 TTCTAAGACCACTTTTAGATGACTCTTATCTGCTAGTAATATTCAATTTGCTGCTACCTGCTTGGTGGTTAGAAG  
 GAGGCTAGAAGATGAATTCAGGCACTTTCTTCCAATAAACTAATTATGGCTCATTCCTTTGACAGCTGTAGA  
 ACTGGATTCAATTTTAAACCATTTTCATGATTTCAAATGTAATTTCTGATTGATTTTAAATGCGTTTGTGA  
 AGAACTTCTGCTATTAGGATGTTTACAGATCTTTATAAGGTGTTTATATATTAGAAGCAATTAATTAACATCTG  
 TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAGTGAAGTGAGATTCTCTGTGCTCATCGGCATTC  
 AACTTTTCTTTGTTTGTGCTCAGTGTGCATTTGAATATGCTGTTTCTATAAATAAATTTTAAAGAATAA

0070103.101501

## FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLALAALLAFVSLQFFHLIPVSTPKNGMSSKSRKIMPDPVTEPPVTDVY  
EALLYCNIPSAERSMEGHAPHHFKLVSVHVFIRHGDYPLYPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVP TKQLRAANPIDSM LCHFCHNVSPFC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQ TIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF  
CQDHHKRS PKMCPLENLVR FVKRDMFVALGGSGTNYDACHREGF

**Signal sequence:**

amino acids 1-18

007003-10504

# FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTCCATCCCCTTTGAAGAACAGTACTGTGGA  
 GCTATTTAAGAGTAATAAACGGAAATATCCTTTCTGGGAGTTCAGATTGTGCAGTAATTGGTAGGACTCTGAGC  
 GCGCGTGTTCACCAATCGGGGAGGAAAGCGGAGATCCTGTCTCGCCTTGCAGCGCGCTTGAGACCAAAAGCAGAT  
 AGCTAGGAAATGAACCATCCTCTGGGAGTATGTGGAAAACAAGGAGGAGCTGTACTTCCCAACTGTCCCATCTTAT  
 GGGCGAAGGAAGCTCTCTGACTTTCAGTGGTTAAGGGCAGAATTGAAATAATTTCTGGAGGAAGATAGAATGAT  
 TCTTGGCGGACTGACCGGGAGCTACAAAGGGCTTGTCTCTGCTGGGAATCTCTCTGGGGAATCTCTGGGAGACCGG  
 ATGCAACCGAGATAGCGTATTCTAGTTTCGGAAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
 GGGGCTGGAGCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGAGCTTTTCGCGCT  
 GAATTCGCGCGAGCGGAGCTTGGTCAAGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCTGAGAT  
 TCAATTAATCTAGACATTTCTGATGGAGGATAAAGTGAATAATATATGGAGTAGAAGTAGAAGTAGGAGATTAAG  
 CGACAATGCGCCTTACTTTTCGTGAAGTGAATTAGAATAAAAAATTTAGTAGAATAACAGGCACTGAGATGCGGTT  
 CCCTTACCCACGCGCTGGGATCCGGATATCGGGAAGAACTCTCTGCGAGAGCTACGAGCTCAGCCGGAACACTCA  
 CTTCTCCCTCATCGTGCAGAAATGGAGCGGACGCTAGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
 CGAAGAAAGGGCTGCTCACCACCTGGTCTTACGCGCTCCGACGGGGCGACCCGCTGCGCACAGGCACCGCGCG  
 CATCCGCGTGTGTTCTGGATGCGAACGACAAACGACACGAGCGTTTGTCTCAGCCGAGTACCGCGCGAGCGTTCC  
 GGAGAAATCTGGCCTTGGGACGACGAGCTGTCTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGGCGAAGT  
 GAGGTATTCCTTCGGTATGTGGACGACAAGGCGGCCAAAGTTTTCAAACTAGATTGTAATTGAGGGACAATATC  
 AACAAATAGGGAGTTGGACACGAGGAGTCAAGGATTCTACCAAGTGAAGTGAAGCAATGGATAATGACAGGATA  
 TTCTTGGCGGAGCCAAAGTCTCTGACTCTTCTGGACGTGAACGACAATGCCCCAGAGTGGTCTCACTCTCTCT  
 CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCGCTTTTAAATGAAATGACCAAGATTCTGA  
 GGAAAAACGACAGGTGATCTGTTTCTATCCAGGAAATCTGCCCTTTTAAATTAGAAAAATCTTACGGAAATTTACTA  
 TAGTTTAGTCACAGCATAGTCTTGGATAGGGAAACAGGTTCCTAGTACAACTACAGTGACCGCCACTGACCG  
 GGGAAACCGCGCCCTTCCACGGAACCTCATATCTCGCTGAACGTGGGACAGACCAACGACAACCCCGCGGTCTT  
 CCCTCAGGCGCTCTTATTCGCTTATATCCAGAGAACAACTCCAGAGGAGTTCCCTGCTCTCTGTGACCGCCCA  
 CGACCCGCTCTGTAAGAGAACGCTCAGATCACTTATTCCTGGCTGAGAACACCTCAGGAGGGGCAAGCCTATC  
 GTCTACGCTGCTCAATCAACTCCGACACTGGGGTATGTATGCGCTGAGCTCCTTCGACTGAGCAGTCCCGAGA  
 CTTGCAAGTGAAGTATGCGCGGGACCAACGGGCAACCGCCCTCCACGAGAGGTTCCTGCTGAGCGGCTGTGCT  
 GGCCTCCCGCTCCGAGAGCCCGGCTACCTGGTGAACCAAGGTGGTGGCGGTGACAGGATCCAGGACACCGCGGACGC  
 CAGCGCGAGAGCCCTGCTGGACAGAGACCGCTCAAGCAGAGCTCCCCAGTCTTGGCGGAGCTCGCAG  
 CCTCTCTCGGCACTGTACGCTCACCCTGCGCGGTGGCCGACAGCATCCCCAGTCTTGGCGGAGCTCGCAG  
 CCTCGAGTCTCCAGCTAACTCTGAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGTGGCGCGCTCTCTG  
 GCTCTCTCTGGCCTTCGTCTATCTTGTCTGGCGCTCAGGCTGCGCGCGCTGGCAAGTCAAGCTCAGCTCTCTGAGC  
 TTCAGGAGGCGGCTTGACAGGAGCGCGCGCTGCGACTTTTGGGCGTGGAGCGGGTGGCAGGCTTCTCCGAGC  
 CATGCTCGTCAAGGAGGAGCTTTGAAAAAGCGAGCCCTTTTGTCTCAGGTGATTGCTGATTTTCAAAGA  
 CAGTCATGGGTAAATTGAGGTGAGTTTATATCAAACTTCTTTTCTTTTTTTTAAATTGCTCTGCTCTCCAAAGC  
 TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCTCAAACCTTAGGCTCAAGCAATATCCACCTTTGCTCT  
 CCGGTGTAACAGGAGCTACAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT  
 CTATCTATCTATCTATCTATCTATCTATCTTGTGACAGCGGAGCTCAACGCTGTAATCCAGTACTTTGGGAGGC  
 CGAGCGGGTGGATCACTCAGGTGGGAGTTTGAAGACCAAGCTGACCAACATGGAGAAACCCGCTCTATATAA  
 AAAAATACAAATATAGCCGGGCTGGTGGTGCATGTCTGTAATCCAGCTACTTTGGGAGGCTGAGTCAGGAGAAAT  
 TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGGCCATTGCACTCAGGCTGGGCAACAAGAGTG  
 AAACCTCTATCTCA

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGLTWETGCTQIRYSVPPELEKGSRVGDISRDGLGLEPRELAER  
GVRIIPRGRITQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELVKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFTIQGNLPFKLEKSYGNYISLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPCDEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSLFLVDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD  
GVQAFQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNCSVSVQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS  
IYLSIYLSIYLSIYLLSCTDGS LTPVIVLWAEAGGSPEVGS L RPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

097573-10504

## **FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCAGTTAAAAG  
GCTCCAGAATCGTGTAACAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTCTGCTCTGTCTGGGGGAGCCTGGGCAGGACACTCCAGGSC  
ACAGGAGGACAAGGTGCTGGGGGTCATGAGTGCCAAACCCATTGCGAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT  
ACAGCTGCCCAC TGTAATAAACCGAAATACACAGTACGCCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTTCACTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCGAGAGAATTTTCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCGAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

007013-14504

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPIVVSQSIHPPCYNSSDVEDHNDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

00766-66366



## FIGURE 160

GGCGCCGGTGACACGGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGGCCGCG  
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGGCCCGCGCCCCG  
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGCCCGCCCGCCCGCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCTCAAAACCACTGATCCCATAAAC  
ATTCATCCTCCCGGGCGGCCGCGCTGCGAGCGCCCGCCAGTCCGCGCCCGCCCGCCCTCG  
CCCTGTGCGCCTTGC CGCCCTTGCACACCCGGCGCCGAGCCAGCCAGAGCCGGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGCGCGCCCTGGA  
TGCGGACCCGGCCCGGGGAGACGGGGCGCCCGCCGAAACGACTTTCAGTCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGGCGTCCGTGAGGGAGCCGGCTGTGTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGTCGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCTGCAACGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGTGGCCCCGAATTGATGC  
GGCTGCCTTCACTGGCTTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCTGCCACATTCACAGGCCTGGGCCGCTACACAGCTGCACCTGGACCGC  
TGCGGCTGCAGGAGCTGGGCCCGGGGCTGTTCGGCGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCTGCAACGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACAGAACCGCGTGGCCCATGTGCACCCGATGCCCT  
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCAACGCCACTCTGGGCTGGCTGCAGAAAGTTCGCCGCTCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCTCAACGCGCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT  
ACTGAGGCCTGGAAGACCAGCTTCGCGAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG  
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCCCTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCGCTCACTGCAGTGCGCCCGAGGGCTCCGAGCCACAGGGTT  
CCCCACCTCGGGCCCTCGCCGAGGCCAGGCTGTTACGCAAGAACCCGACCCGACGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCCTGCAGCCTCACCCCCCTGGGCTGGCGTGGTGCTGTGGACAGTGCT  
TGGGCCCTGTGAACCCCGAGCGACACAAGAGCGTGCTCAGCAGCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGGCGCGACCCGTGGGGCAGGCCAGGCCAG  
GTCTCTCCGTGAGGACGCTGCCGCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCCGCGCAGCGTTTGTTCAGAACCGCGCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGACGACGTGGAATAAAGAGCTCTTTTCTTAAA  
AAAA

05973437-101504

## FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184  
><subunit 1 of 1, 473 aa, 1 stop  
><MW: 50708, pI: 9.28, NX(S/T): 6  
MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCGLELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRRLNDNPWVCDRCRAPLWAWLQKFRGSSSEVPCLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSGSGALPSLTCSLTPLGLALVLWTVLGPC

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Leucine zipper pattern.**

amino acids 135-156

#### **Glycosaminoglycan attachment site.**

amino acids 436-439

#### **N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

#### **VWFC domain**

amino acids 411-425



## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLIQRQQLVFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVS RGNKHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLESFPFEFFQAEQLV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVTGTVNGEISYSLFQASEEIGTKFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPLMLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTAQVYISLLPPQDP  
HLPLTSLVINADNGHLFALRSLDYBALQGQFQFRVGASDHGSPALSSAELVRVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGDGSGQAWLSYQLLKATELGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAO  
ADLLTVYLVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNPPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

**Abstract**

ACCACACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCGCGTAGCGGTG  
 GCCGATTGCTCTCGGCTGGGCAAATGTGTCCGGCTGCCGGTGCAGACACGCCCCCGCGTCAT  
 GCGGCTCCTCGGTGTGTGGCAAGTATTGCTGTGGGTGCTGGGAC'TTCCCGTCCGCGCGGTGG  
 AGGTTGCAGAGGAAAGTGGTGCCTTATGTTGCAGAGGAGCAGCCTGCTCACCCCTCTCCAGGTG  
 GGGGCTGTGTACTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
 AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCAGGCGATCACATGGTGATGCTGTCTG  
 TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTGAGGCCTAGCGGCGTCACCTGTGGTGCT  
 GGAGGAGCGGAGGACTCAAGTGCAACGCTCCGAGAGACCTTTTCTCTGTGATGGCGCTGG  
 AGCACACTTCCCTGCAGACAGAAGAGAGTATTACACAGACAGAGAAGTGCGGAATCTGACG  
 CAGCCCTGCAGAGGACTCCAATAAGCACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
 GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT  
 TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTTACACCCGTTGGT  
 GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
 CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
 TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC  
 GAACACTGGAACACTGAAAATCTTCATT'TTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
 GTGGTGGTAACTCAAGCCGACCAAAATAGGCCTCTTCCAGCACTTTGATAAAAAGTGTGGA  
 CTGGTTGCTGTATTTTCCCTATTCTTTTAAATAGT'TTTATTATGTATGCTACCATTCGAA  
 CTGAGAGTATTCGGTGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
 GAAAGAAGTTGGAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
 CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAGAATCATT'TGTTGAA  
 CACTGTAATGTATAAAAAATTATAAACTGGTGT'TTAACTAGTATTGCAATAAGCAAAATGC  
 AAAAAATTCAATAG

## FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEEL  
ELLHDPMGQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAPTEDSNNTESLKSPPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNMGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILFQGAQPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCTCTGCGCTCGCACTGCTGCTGGGCTCGGCGCGGGGCTCTTCTCTC  
TTTGCCAGCCCGACTTCTCTTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTGTGCTCGCTCTTCCCCCGCTGCGCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGGGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACACCTCCTGCCAGCCACCGAGGAAGCTCCAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCACTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCTATCTGGTTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGTCTC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCTAGCTGCTCCAGTCTCAGCCTGGGAGCT  
TCCCCCTGCC'TTTTGCACGTTTGCATCCCCAGCATTTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAACATAA  
AAATCATGAATATTTTAA

## FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSAAGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLCVQVKDR  
CAPVMSAFGFFWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSEKDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGELVITSVKRWQKQREFKRISRSIRKLQC

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

0076193-101501



## FIGURE 168

GTGGAGGCCGCCGACGATGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCAATTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGGGGCTCCGTGCGGGC  
ACCATCCTGGGTGCGTGGCTGAACCTTTGCCGGGAGTGTGCTACGCATGGTGCCTTGCACTGGT  
TGTTGGGACCCAAAACCCATTTGCTTCCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCACAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTCGAACCCCTCTGGGCGTCTTGTGGCCAATGTGCT  
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCAACCCG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAAACAAGGCCATATGTCTCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTTC  
GGCCTCTGTGGCGCTCTCTTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA  
GTGTTCTTCCCCGTGGGGGAGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGTGATGGCCGG  
CCTGTGCACCTTCTTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCAGCGGCACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCACGACGCCAGCGCCCTCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGTGGGTCTCACTCCTCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

0978493-104504

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLV  
KKGEDIPMLGVYTIPAGVVCLLSTICLWESVPEPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQLQGQTLALAATCSLLGLFGFSVGFVAMELAVECSFPV  
GEGAATGMIFVLGQAEIGILIMLMTALTVRREPSLSTCQGGEDPLDWTIVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

# FIGURE 170

GTCCCACTCTGCTCAACTGGGTGCTGAGTCCCTCTTAGACAGCTCTTGTCCATCATTTGTGTAAGTGGACCAAC  
TAGTTCCCAGTAGGGGGTCTCCCTTGGCAATCTTGTAGCGGGTTTGGACATCTCAGATCGCTTCCATGAAGA  
TGGCCTTGCCTTGGGGTCTCTGCTTGTTCATATCATCTAATATGAGGACAAAGTTGTGCGGGCAGCTCTTGGGGG  
AAGGAGCACTGGGGCTGATGAGCAATCCAGGAACCTGGAGGACTTGTCCAGCTTGGAAAGACTCTAGTGTGT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCAGGTGTG  
CTACTTATTTCTTTTAGGGGATTTGTGAGGAGTGACCACTCTCAAGTGAATACCAAGTGTGAGAGGAGTGCCT  
ATCTGTGTACAGTGTCTGGGAGCACTGTGCCAGAACTTGGCCGGAGGAGAGCGGAGCTTGGGGCGCCTT  
CCAGGTGTGTGAGCTGCTGAGGCGCTCCCAATCAGGTGGACTCTGAGGAAGGCTTGTGACAGCAGGCGAGG  
GTGGATCGAGAGCAGCTGTGCCAGCAGTGGGATCCCTGCTGGTGTCTTGTATGTGCTTGGCCAGGGGATTT  
GGCTCTGATCCTGATGTGGAGTCTCAAGTGTGAGCAATCAATGACCAACAGGACAGCGTTTCCCAAGGCGAGCAGGA  
GTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGAGTCCCTGGACAGGACTTGTGACCCAGACACAGGCCCC  
TAACACCTGACACCTACACTCTGTCTCCAGTGAGCACTTGTCTTGGATGTCTTGTGGGCCCTGATGAGAC  
CAACAATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCATTTTGTATCTGGTGTAACTGTC  
CTATGACAAATGGGAACCCCCCAAGTCAGGTACAGCTTGTGCAAGTCAAGCTTGTGACTCCAAATGACAAATAG  
CCCTGCGTTTGTGTGAGAGTCTCACTGGCACTGGAAATCCAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCAGACAGCTGACAGGCCCCAATGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCTCCAGAGGT  
GCTGGACACTCTCAGTATTTAGTGAACAGAGCAGGCTGATCTTGTGCTGACCTTAGACTAGAAAAGAACCC  
TGCTCATCGAGGTGGATGTTTCAAGCAAGGAGCTGGTCCCAATCTATCCAGGCCATGCAAGTGTCTCATCAA  
GGTTCTGTGATGTCAATGACAACTCCCAAGCATCCAGCTCATAGGCTCCAGGCTCATCTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTATGTCTTGTCTATGAGCAGTGTGATTCAGGACCAATGGTTTGTGTCATG  
CTGGCTCCGAGCGACAGCTGTGGCCTTCAAGCTGAAAGAACTAATGGCAACATACATGTGTGCTAACCACTGC  
CAACTGAGCAGAGCAGCTGGCCCAAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCGCTTATC  
AGCCAAAGAACAGCTCAGCACTTCAAGTCACTGACATCAAGCAACATGCACTTGTGTTGAGAAAAGCAGGTATGA  
AGTCTCCACGGGGGAAACCACTTACCTCTCTCACTCATACCATCAAGGCTCATGATGACAGCTTGGGCACT  
TAATGAAAAGTCTCATACCCGACTCCAGGACTCCCACTTGTCTTGTAGTGTGATCTGACTCAACACAGGAGA  
GGTCACTGCTCAGAGTCTCACTGAATATGAAGAGATGGCGGCTTGTAGTTCCAGGTGATCGCAGAGGACAGGG  
GCAACCTGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCTTCTGTAAGTGCACATGATGAATGGCCAGAGGTGT  
CCAGCTTGTGCTCAGGATGGAAAGCAGGCTCTCTGCTGTGTGAATGCCCTCACAGGCCACCTGCTGTGTGCC  
CATCGAGACTCCCAATGGGCTTGGGCGAGCTGACACACCTCCATGGGCACTCACAGCTCCCGGCAAT  
CCTTTTGACAACTTGTGTGGCAGAGATGACAGCTCGGGGCAATGAGAGGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACTCTTCACTCTCAACCTCATACGGGCGAGCTGTTCCTCAATGTCAACATGTCCAGCAGCT  
CATTTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGAGCAGGGAGGCCCTTACAGACCCGAGCCTGTGT  
GAGGTGATGTTTGTACCACTGTGTGACCACTGAGGAGCTCAGCGCGGAGCTTGGGGCTTGGACATGTGCT  
GCTGACGGTGTCTGCTGGCTGTACTGTGTGGGCTCTTGGGTTGATCTGAGCTTGTTCATGTCTCTGCG  
GACAGAAAAGAGGACAAAGGGCTCAACATGTGCGGAGGCGGAGTCCACTACCGCAGCAGCCCAAGAGGCC  
CCAGAAACCAATTCAGAAGGCAGACATCCACTCTGTGCTGTGCTCAGGGGTGAGCAGCTGAGCTTGTGAAT  
CGGGCAGTCCCAAGAGTGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGAGCCCTGCTGCAAGCCCTT  
CCACTCAACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAAGGAGCACCCTGGGAGAGCCGAGAGGT  
GCTGCAAGACAGCTCAACCTCTTTTCAACCTCCAGGCGAGGAATGCCCTCCGGGAGAACCTGAACTCTCC  
CGAGCCCGAGCTGCCACAGGCGAGCAAGTCTCAGGCTTGTGAAGTTGACAGGACCCCTGAGGAGGCTGGC  
TGGAGACCAAGGCGAGTGAAGGAAGCCCCACAGAGGCCCAAGGCTCTCTGCAACCTGAGACCGGAGCAGCAT  
CAATGGCAAAAGTGTCTCCCTGAGAAAGATCAGGGCCCCGTAGATCTCGGAGGAGCTGGTCCGGGTCTCTGTG  
TGCTTCTGCGGAGCGGAAACCCCTGGAGGAGCTCACTGTGATTTCTCTCTGTGTCAGCAATCTCCAGCTGTCT  
GTCTTCTGTGATCAGTGGCCCAATTCAGGCCAAACCAACCCAGGAGAAATAGTACTTGGCCAAAGCCAGGAG  
CAGCAGGAGTGCAATCCAGACACAGACTGGCCCAAGTGCAGGGCTGGAGGCGAGACAGACAGCAGGAGGAG  
AGGGCTTTTGTGCTTGAAGAGCACTCTCTGTGAAGCAACTGTGATGAAGAGAGCTGTCAAGTCTGTGTGAGCC  
CAGCAGAGCTGTGCCCTGGACCGGCTGAGCGGCCCTGACCGGCTGGATGGCAGAGCTCTCTTGTGCCCTTAC  
CACCACACTCGTGACAAATGTGATCTCCCGGAGCTGTGACGCAAGGAGGCGGAGGAGCTTCCAGAGCTTCG  
CAGGCGAGGACCAAGAGCTGAGGCCCAAGGACAGGAGCTGGCGGAGCAGCTTGTCTGAGAGTGAAGTCACT  
GCTGGAGATGTCTGTGAAGCAGCTCCAGCTGAGGCGCGCTCCGAGGCGCTCGGGCGGCTCTCTGCT  
CTGCGGGAGGACCTCAGTTTATAGCTTGGCCCAAGTGTGAGCTCAGGCTGAGGATGAAAGTCAAGGGGACCCAGGTG  
AAGAGCGGGGACTGAGGGCTGAGGACGAGGCGAGCAGCAGCAGGAGGAGGAGGCTGTGATGACATCACTCAGCGCT  
CTGATCTCAAGAACAGGGGCTGAGGATCTGTGGAACAGAGCTGGTTTCAAAATCTTGTAACTCACTAGCTGAC  
CGCGGCTGTGAACATTTAGGTGACTGATGCTACCCCAAGGAGGAGGAGGAGGAGGAGTCAACAGCTGAGC  
TGACCAAGACAGCCCTTGTGAAGCAGCTGTGATCTTTTGGAGGACAGGAGCGGTTTGTGGCTGAGATGAAGTGT  
TCTCTGGAACCAATCTGTGGACCAAAAGGCTGAGTCTCTGCGAAGACAGATGACCGGAGTATCAAGGGG  
AAAGGTTGGCTTCTTGGTGTAGCAGGAGTCAAGGGCTGTACCTGGGGGTGCGAGGAAATGCTCTGTGACCTAT  
CAATAAGGAAAGCAGTAAAAA

## FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLLQLLLGLLPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTIVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRDLREQLCRQWDPCLVSFVDLATGDALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPDLRALDPDTPNTLHTYTLTSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS  
LALEIQEDAAPGPTLLIKLTATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDNDNIPSIVHTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVTRENNLPSLHLITIKAHDADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPM LassVS VWVSL LLA  
NDNAPEVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPPLATHSSRPFLTT  
IVARADSGANGEPLYSIRNGNEAHLFI LNPHTGQLFVNVTNASSLIGSEWELEIVVDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPLRGQAGEPCEVQSHKDV DKEAMMEA  
GWDPCLOAPPHLTPTLYRTLNRQNGGAPAESREVLQDTVNLLFNHPRQRNASREN LNLPEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAQRP PASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGS  
RSAIPDTDGPSARAGQTDEPQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDGPGKGTGTEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563



## **FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFPMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPFIPILSPKHGILSIEQLISRVGVIQVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGGIIIVTSIRGLLITLTFFFYAISS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

097037-1500

## **FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAAATGAACCTGTGTGTAATTC TGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCAG

0978193-101501

## **FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAAATTGGCCAAGGGTTTC  
TTTNTTGAATTCGGGTNNNGNATACCTTCCAGAAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTCATGGTGCCFTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAN  
TAGGAGATCCCTTTCCCATTC

00705-1110





## FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPPWAGSGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGFLFACPLSLEETDCYRVDDIDQGADMQKESKENQWL  
GVSVRSQGGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFCBG  
RPQGHEQFGFCQQGTAAAFSPDASHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPLYEA  
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTS GFGYSLAVADLNSDGWPD LTVGAPYFFERQEELGGAVVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGD LNDQDGFDPDIAGVAPFDGDGKVFIYHGSSLGVVAKPSQVLE  
GEAVGIKSGFGYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRCVFSYIAVPSYSPTVALDYVLADTDRLRGQVPRVTFLSRNLEBPK  
HQA SGTVMWKHQHDRVCGDAMFQLQENVKDKLRAIVVTLVSLQTPRLRRQAPGGQLPPVAP  
ILNAHQ PSTQRAEIHFLKQGCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPADGDDAHEAQLLVMLPDSLHYSVGRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYLI LSTSGISIEETLEVE LLLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEYEVTVSNQGSRLRTLGSAPFLNIM  
WPHEIANGKWL LYPMQVELEGGQGGPGQKGLCSRPNPIHLHDVDSRDRRRRLEPEPQEQQEPGE  
RQEPMSWVPVSSAEKKKNTLDCARGTANCVVFSCLYSFDRAAVLHVWGR LWNSTFLEEY  
SAVKSLEIVIRANITVKSSIKNLMRLDASTVIPVMVYLDPMMAVVAEGVPWWVILLAVLAGLL  
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKBEKTGTILRNWNGSPRREGP  
DAHPILAADGHPGLGPDGHPGPCTA

### Important features:

#### Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 1040-1062

#### N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

## FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAAACAAGATGCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGCGGTGCGACGGCGGTAATTTTC  
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCCTTCAGATAAGCCCAACAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAAGGAAGTGGCAACAGATTGCGGGACTGGTTCAGGCCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTTAACAGACTTGATACAAACTATGACCT  
GCTATTGGACAGTGCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCTATGGCAGTGTGGACAGTGTGCTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTGAGTTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAATTTATCTTCTCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAAGCTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTATATATCTTACACAAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTGAAGTGCTACTATAATAAAATTTTTACAGAGAACAACTTTGT  
AAATCTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG  
ATAATTCTAAGTGAAATTTAAATAAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

0976193-107504

## FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPCVVYVSPVCGSDGHTYSFQCKLEYQACVLGKQISVKEGHCPCP  
SDKPTSTSRNVKRACSDLEFREANRLRDWFKALHESGSONKKTLLRPERSRFDTSILPI  
CKDSLGMWFMRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKLLGQYIPLCDEDEGYKPTQCHGSGVGCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEDEGDDDDGGDDHDVYI

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

# FIGURE 180

CAGACTCCAGATTTCCTGTCAACCCAGGAGTCCAGAGAGGAAACGGGAGCGGAGACAAACAGTACCTGACGC  
 CTCCTTCCAGCCCGGATGCTCCCCAGCAGGAGTGGGGGACAGATCTGGCTGCCTTCCCCTGCTCTCTGTGGCC  
 GCTCTGCTCCGGTGCTGCTGCTGCTGGGGCGGCCGCTTACACCTTCCCTCGATAGGACCTTACCCTTTACCTCT  
 CCGCGCGGCGCAGAGAGGAGTGCTTCTACAGCCCATGCCCCCTGAAGGCTCGCTGGAGATCGATGATCCAAAGTTT  
 GATGGAGCAGGATTAGATATTGATTTCCATCTTCCCTCTCAGAAAGCAAACCTTAGTTTTGAACAAAGAAA  
 TCAGATGGAGTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAAATACATTCAGCCAAAT  
 TCTGAGAAAGTGATTTCCTTTGAATTAATCTGGATAAATATGGAGAAACAGGCACAAAGAAAGATTGGAAAG  
 AAATATATTACTGGCAGAGATATATTGGATATGAAATCGGAAGACATCTCGGAATTCATCAACAGCATCAAGTTC  
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAGAAAGCC  
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAATTTAGTGGTCACTGGTGGTGGTTCGACCACTCAAGATTAT  
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAACCTCCAAACATAGATACGTAACTGATTA  
 AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
 AAAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTCTGTGCAAGTAACTCTGTGATCCAG  
 TTGTACTTAAGTGTGAACAGGAATATTTGCGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAAT  
 TTTCTTAACTTTGAAAAATTTTGCAAAATGCTTAGGTGATTTAAATAAATGAGTATTGGGCCCTAATTGCAACACC  
 AGCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTGTAAATCGCGGAGTTACAAATTAAGCTGGGAAGTTT  
 TACTTTTTTAAGTTTACATTTACCTGTGAGAAATTAACCTAATGATGGATTGAATAAATCTTTAGATACAAAAGCCAA  
 CTTTTCTCTATTATACATATGACTCTCTCTATAATGTAATAGATAATAGCTTTGAAATACAAATAGGTTTGTG  
 AGATTTTTATACCAAAATCAATTTCAAGTGAACATATTAGCAAGAACATAGCTTTGTACTTTGTCTTACCTTTG  
 CCAAAGCTGACATTTTCAAGATCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
 AAATGAAGAAATATAGTTTAAAGCTTCCCTCCATAGGGACACATTTCTCAACCTTAACTAAAGTGAAGTTT  
 TTTTAAATTAATGTGAGGTAAATTAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
 TAATCATGTTATGTTAAATTTTAAATGATGCTGACTTGGATAATCTATTAAACAGAGTTATGAAGGAAATA  
 TTGCTAAATGATCTGGGCTTACCATTAATAAATATCTCTCTTCTGAGCTTCAAGAAATATACAGAAACAGGAA  
 AGAATTTAGAAAACTTGAAAAACCTAATCCAAATAAAATTAACCTTAAGTAGAACTATAAATAAATATCTAGA  
 ATCTGACTGGCTCATCATGACATCTTACTATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGGAG  
 AAATCTTGGCTGAGTGTTTTTATTTTCTACAGAAATCTGGTTTGAATTTTGTGAACAGGTATGTTTTATA  
 AAATGTAAAGCCCTACTGTAAAGTTTAGCACTGGGTGATACATTTTATAAAAAATTTTATATAACAATTTTAT  
 TAAAAATGGCCTTCTGAACACTTTATTTATGATGTTGAAGTAAGATTAGAAACATAGACTCCCAAGTTTATAA  
 CACCTAAATGTGAATAACCCATATATACACAAAGTTTCTGCACTCTAGCTTTTGAAGCTATGGGGCTCTTAC  
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAATTAATTTTAAAGTTATGCCATTTATAACGTTGTTAT  
 GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAAGAGTTATGATGCTGGAATTT  
 CTTGATGAGCAATAATGATAACAGAGAGTGATTTCAATTAACATCATAGTAGTATAAAAGAGATACATTTCCC  
 TCTTAGGCCCTCGGGAGAGAGCAGCTTAGATTCCCTACTGGCAAGGTTTAAAAAATGAGGTAAATGGCCGTAT  
 ATGATCAATTAACCTTAAATGGCCAAAGAAATGCTTCAGGTGCTCAGGGGTATCCTCTGCAACACTTCGACAAACA  
 AGGTCAATAAGATCTTGCTCATGAATACCCCTCCCTTTTGGCGTGTAAATTTGCAATGAGAAGCAAATTTTACA  
 GTACCAATACTAATAAGCAGGGTACAGATATAAATCTGTCATCTTTCTATAAAACCTGTGATTAAGAATTTCTA  
 CCTCTCTGTGCTGTTACTGTACTGTACTCTGACTCTCTACCTAACAAATGAATTTGTTACATCAATCTCT  
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCAGTAACCTTCTTACCATATAAAACGATTAATGCTT  
 TATTTGGAAAAAATTTAGGAATCTAAGGACAAATTTTATAGACAAAGTAAAAAGACAGATTTTAAAGAGG  
 CATAACCAAAAAAGCAAACTGTAAACAGAGTAAAAATCTTAAATATTCTTAAAGACATACTGTTTATCTGCTT  
 CATATGCTTTTAAATTTCTGATTTCCATTTCTAAATTAAGGTTATGCTTAAATGAGTAAGCTGTTTATCACTT  
 AACAGCTCATTTTGTCTTTTTCATATACAAAATTTAAAAATACTACAAATTTTAACTAAGGCCCAACCGGATTC  
 CATAAGTGAAGTTTACCGTGTCTCACTCAACACTAAGGCCATAGGTTTGTCTCTGAATGCAATTTGGATGTAAT  
 GTTATGCTGTTCTTCTCATGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGTTGAAAAATTAATCTCTTCA  
 GATAGATGGGTCTTAAAAATGACAAAAATGAGCACTTCAAAATGATGCTCCTCAATGAAGCTTCTTAT  
 CTCGAAATTTAAAGACATGATTTCGCGATGTAGGATTTTCACTGAGTACAAATATGCAAAATCAGTGTG  
 GTCAAATGCTTTTATACCTTATAAACAGCCATCTTAAATAGCAACGTATTGTGAGTACTGATGTATATAATAA  
 AAATTTTCAAAGGAAAA

0976193-101601

## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196  
><subunit 1 of 1, 229 aa, 1 stop  
><MW: 26017, pI: 4.73, NX(S/T): 0  
MGDKIWLPPFVLLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY  
QVLGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFTSTISEKVIFFEL  
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDVRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

## FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTTGGATG  
CTGCTTTCTGCCTCATTCTCCTGTGTGAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCTTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC  
TTCTTTTCTCTTTTCTTACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

0078703-424504

## **FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKPKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

007073-0000



## **FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCAGGGGGACTCCACGGTGACCAAGTCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCTGCACCAGGAAAAAAAAAAAAAAAAA

007693.101504

## FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKITLYSREIVYP

FQGDSTVTKSCASKCKPSDVGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

0076193-10544

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCGGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCCACCGCGGAGGGGACGCAAGCGCTGCAAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAAAG  
CTGCATGCGTCACGCTATGTGCTGCCCGGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATGTGTGTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAAGAGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCT  
TTGCGGATACAGAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAAC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAAGGCTTTGTTTCTTATGGAACCTCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAGCATACCCCTTTACCCCATTAATTCTAGAGCTAGAACGCA  
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

## **FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIIDNYQFYPCAEEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKRRRGKSGHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

00000000000000000000000000000000

TGTGTTTCCCTGCAGTCAGAAATTTGGGACNCGAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGCGCGGCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTT  
AATTCCAAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGACCCAGGNTT  
TGCAGTCAGCGCCGCGCGCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAAATNTGNTNNGCTGCAGGAAGCGCCGAAAAACG  
CTGCATCGCTCANGCTATTGTGCTGCCCGGGAAITACTGCAAAAATGGAATATGTGTGNTT  
CTGATCAAAATCATTTCCGAGGAGAAATGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCAACTGGATGGG

# FIGURE 189

GAGGAACCTACCGGCTACCGGCCGCGCTGGTAGTCGCGGGTGTGGCTGCACCTACCAATCCCCTGCGCGCGG  
 CTGGGCGCTCGAGAGTGGCTGTGCTTCTCTCTGCACGCGGTGCTGGGCTCGGCGAGCGGGGCTCCGCCCA  
 GGGTTTAGAGTGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTGTGGAATGAAAGGA  
 AGTATTGAAATGAGCTGAAACCACTTACAGATTAAATTTTGGGGACAGATTGTGTATGCTTGATTCACTT  
 TGAAGTAACTGACACAGAAGTTCTCAAATTTGCATATTACATCACTGGAACCGAGCTGAATCTTAATGTTCAC  
 TTAATCAGAATCTGCAATGAAAGGAATGGAGCTCGGTTAAATAAAGATGACATATCAGACACTTGAAGAAG  
 GATCACTCTCTGTTTTCTGATAGTGATATGGCCATTTTAGTGGGACAGATCAGAGATTTTTACAGTTTACTCTGAT  
 AGTGTCCAAAATCGAGAGCAGTAGAGAAATAGACAGCTTTTCAAGAAATTTGGCATTTGAAGTTACATCTGATTA  
 AAACCCGAAATAACCAAGTGACACTGGCGATTTTAAATAAATAAGACATATGAAGTACTCAAGATGAAGA  
 CTCTAGGAAAGATGACAAATATGGAGAAAGGAGCTTGAAGGATAACAGGTGGCCAGTATGAAGGTGGAA  
 CTATTATCGTTATGATTGTGTATTTATGATGATGATCTGAAATCATAACTTGAAGAAGAGAAATTTGATGT  
 TGCTGTTAATTTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCAGGCTGTTCACACTGCCATGATTAGCTCC  
 CACATGGAGAGACTTTGTAAAGAAAGTGGATGGGTACTTCGAATTTGGAGCTGTTAACTCTGGTGATGATAGAAT  
 GCTTTGGCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTCATTTTTTGGTCTGGAATGGCCCCAGTGAATA  
 TCAATGGAGACAGATCAAGGAGAGTTTGTAGATTTTGAATTTGCAATGAGACATGTTAGAAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCAACTCCATCAAACTGCTTTTGTCTGTGGTATTGGCTGGGTGATCACTTTTGTGTCAA  
 AGGAGGAGATTGTTGACTTCAACAGACAGCTCAGGCTTAGTGGCATGTGTTTTCTCAACTCATTTGGTGCTAA  
 AGGATATATTTGGGAGTAATACATAATCTCCAGATTTTGAACACTCTTTGGCAACACACTAGAGAGTCTGTTT  
 GGCTCATCATCGGTGGCTGTATTTTTCATTTTGAATAAATAAGAAATCAAAATGATCTGAGCTGAAAAAAT  
 AAAAATCTGCTTAAATAATGATCATATTCAAGTTGGCAGGTTTGAATGTTCTCTGACACAGACATCTGTAGTAA  
 TCTGTATGTTTTCAGCGCTCTCTAGCAGTATTTAAAGGACAGAGAACCAAGAAATGAAATTCATCATGGA  
 GAAGATCTATATGATATACTTGCTTTGGCAAAGAAAGTGTGAATTTCTCATGTTACACAGCTTGGACCTCAAA  
 TTTTCTGCCAATCTCAAGAACCATGGCTGTGTGATTTCTTTGCCCCCTGGTGTCCACATGTGCGAGCTTTACT  
 ACCAGAGTTTCAAGAGAGCATCAATCTTTTATGGTCAGCTTAAGTTTGGTACACTAGATGTGATGCTCATGA  
 GGGAGCTGTGAATGATAAATCTCAGGCTTATCCAAACAGAGGTTTCAACCACTCAACATCATGATGATGA  
 TGAGAGCACTCACTCTGCTGAACAAATCTTGGAGTTTATAGAGGATCTTATGAATCTTCAAGTGTCTCCCTTAC  
 ACCCAACCTTCAACGAACTATGTTTCACAAAGAAACCAACAGCTTGAATGGTGTGATTTCTATTCTCCGT  
 GTGTCTCTTGGCCAACTTATGTCAGAGATGGAAGAGTGGCCCGGACATTAATGAGATGATCAAGGTGGG  
 CAGTATAGATTGCCCAACAGATATCTTTTGTGGCCAGGAAACGTTCAAGATGATCCCTGAGATGAAGATTTT  
 TCCCCCAAATCAAATAAGCTTATCAGTATCAAGTACAACTGGTGGAAATAGGATGCTTATCTCTGAGAA  
 CTGGGCTTAGGATTTTCTACTAAGTATCCAAGTCTCAACCTCAGACTTTCAAGTGAAGAAAGTTTCTCAAGG  
 GAAATCATTTGGGTGATGATTTCTATGCTCTTGTGTGGAAGTCTGCCAGATTTTGTCTCAGATATGAGCT  
 CTGCGCTAGGATGATTAAGGAAAGCTAAGCTTGAAGTGAAGAAAGTTTAAAGGAAATTTGACAGATGACATCAG  
 AGCTGGGATCAGGCTATCCAGCTGTAAAGTTTATTTTCTACGAAGAGCAAGAGAAATTTTCAAGAGAGCA  
 GATAAATACAGAGATGCAAAAGCAATCGCTGCTTAAATAGTGAATAATTTGAAACTCTCCGAATCAAGGCA  
 GAGGAATAAGGATGAACCTTGATAATGTTGAAGATGAAGAAAGTTTAAAGGAAATTTGACAGATGACATCAG  
 AAGACACCTATTAGAAATGTACATTTATGATGGGAATGAATGAACATTTATCTAGACTTGCAGTTGTATGCCA  
 GAATTATCTACAGCATGTGTGTAATAAGAGGGTCTGCAAACTTTTCTGTAAGAGGGCCGGTTATAAATATTTTA  
 GACTTTGAGGCTATATATATGTTTCAACATGAGAACAGAAATGAGTATCATGTATGTTTGTATTGTCT  
 TTTAACCACTTTAAATAATATTAACAGATTTTATGCTCAGAGCCATCAAAAGTATGCTTGGATTCAGTCCATG  
 GACCATAGATTGCTGTCCCCCTCAGCGGACTTATAATGTTTCAAGTGGCTGGCTGAACATGATCTGTCTGTCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTTCCCTTCAAGTTTGTGGCTGACCTGAAAGAGGTAAC  
 TAGTTTGTGTCAGTTGTTCTCTCAAAATGCTATCCCTAACCATATATTTATTTTGTGTTTTTAAACACCCAT  
 GATGTGGCACAGTAAACAAACCCCTGTTATGCTGTATATTAATGAGAGATTTCTCATTTGTTTTCTTCTCTCA  
 AAGGTTGAAATAAGCTTTTAAATTTTCAACGCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAAGTACAC  
 AAATTTGAGCAACAGTAAAGTGCACAAATCTGTAGTTTGTCTGTATCATCCAGAGTGAATTTTGTAGGCACTCAAT  
 TAGCAATTAATCGGCAATGTAGAGTATCTCAATAATGTTATCAAGTATTAGAGTTCTATATTTTAAAGATATA  
 TGTGTTCTAGTATTTCTGAAGTGTCTTTCATAGAAATTTTCCACTGATGATGATTTTGTAGGCACTCAATAT  
 TTACATATTTGCTTCTGAACTTTGTTTGAACCTGTATCTCTTATTTACATTTGGGTTTGTCTTTTCAATGTTTGG  
 TTTTTCACCTGTCAGGCTATTTATTTATCAAAATAGGAAATAATCTTTACAGTGTGTTTACAGTGTAGCTTAT  
 AATGATGCTGTAGTTTATCCAGTTACTAGTTTACTGTGAGAGGGCTGCTTTTCAAGTAAATATGACATAAT  
 CAAGTACTGTTATTTTAAAGAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA  
 CTCAAGAAATCACAAAATTTGTCAGTAACTGTAGTTGTTTGTAGTTAATTCAGAGGTGACAGAAATGTTAAAT  
 CCAATCAGTCAAAAGAGGTCATGAATTTAAAGGCTTGCACTTTTCAAAAAAATAAAAAA

## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDAQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNPNNAHGDFLKNINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGI  
YDDDEPIITLERREFDAAVNSGELWVFVYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSVTVELWTGNFVNS  
IQTAFAAGIGWLITFCSKGGDCITSQTRLRLSGMLFLNSLDAKEIYLEVIHNLDPDFELLSAN  
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLVVFQF  
SLAVFKGQGTKEYEIHGHKKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVSILTPTTFNELVTQRKHNEVMMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPBPELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKATAALISEKLETLRNQGRNKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCTCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGTTCTGTGGGATATTAAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTGGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTGGCTTTCACAGAGGTCTGACATCAGAAGTTTCTAGGCTT  
GGGAAAAAATGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCCACA  
AAAATCCAAGCAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAAATGATTTTTTGTTCATCGTATATCAATATCTTCTGAG  
ACTACAGAAGTTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG  
TATGCGATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTT  
TCAGTCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACCTTAAAGGTTTTCTTTAAGATAT  
TTTATTTTTCCATTTTAAAGGTGGACAAAAGCTACCTCCCTAAAGTAAATACAAAGAGAACT  
TATTACACAGGGAAGGTTTAAAGACTGTTCAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAAT  
TTTAGGCTCAAAAATTAAGCTTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAGAGAAGAA



097293

&lt;MW: 33655, pI: 9.31, NX(S/T): 1

amino acids 1-19

2

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

## FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCACAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCACGCCCGCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGTCTGGGGTCGGTGTTCATGATCCT  
GCTGATCATCGTGACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCACACGCCCGGGCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCC CGCGCAGCGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGACCCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCGCGCGAGCA  
CGTGCAACAGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCCCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCTGTCGCGGACCCC  
TTCGTGCGCCTGATCTCCGCTTCCGCGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCTGTTGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACTCTCTCC  
GAGACTGAAGCTTTCGCGTTGCTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCCTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTAAAGATTAAATATATTTCAGGTATTTAATACGA

CG73493-101504

## 0978-0133-101507

MTKARLFRWLVLGVSVMILLIIIVYWSAGAAHFYLHTSFSRPHTPGPLPTFGPDRDRELT  
DSDVDLFDLDFSLAGVKSQDLPRKETEQQPAPGSMEEVSVRGVDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFFPKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVIMVLS  
GSLLRHGAOPYRDLPIPREHVVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELNEVEYRKFVAPMLRLYANHTSLPASAEAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQYFLRCHPCQIDYDFVKGLETADASAQQLQLQVDRQLRFPSPSYRNT  
ASSWBEDFAKIPLAWROOLYKLYEADFVLFGYKPKENLLRD

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

REF ID: A63927

TCCGGGCCAGAATTCCGCACGAGGCGGCACGAGGGCGACGCGCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACACGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGCGCGGG  
CCTGGAGCAGGAGCTCCCTGGAGCTGCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCTTGGTTTCTGAGACCATCCGCCGATTGGCCGCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCACAGAGGCTTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGGAATGTATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTTGGCAGCCTTAATGCCAGACCTTAGGGCCACAATCCGAGAGGGCATGCTGGCCGAG  
CCACTGGGCCGCTATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGTCCGACAGCTGGGGTAGCGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCGATATCCCTCTGTGATTCTCTCATT  
CTACTTGGGGCCCCCTTCTTAGGACTCTCCCAACCCAACTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCTTAGACTATAAGCCAGTTAGCAAGGTGCGGGGTACCCCTGCAGGTTCCCAT  
AAAAACGATTTCAGCC

## 0978193761014

&lt;subunit 1 of 1, 270 aa, 1 stop

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVI CDKDESGGRALEQELPQAVFILCD  
VTQEDDVKTILVSETIRRFGRGLDCVNNAGHPPPPQRPEETS AQGFRQLLELNLGTYITLTKL  
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVVNCISPGN  
IWTPLWHEELAALMPDPDPRATIREGMLAQLGRMGQPAEVGA AVFLASEANFCTGIELLVTTG  
AEFLYGCKASRSTPVDADPIES

N-glycosylation site.

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGACAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCA CGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCGCCG  
CCTCTGCCCCCACC GCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

0076493-101501

**FIGURE 198**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294
```

&lt;subunit 1 of 1, 180 aa, 1 stop

&lt;MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQRPGLAPGHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDSRIPVDLPEARCLCL  
GCVNPFTMOEDRSMVSVPVFQVPRRRCLPPPPRTGPCRQRAVMEETIAGVCTCIF

### Important features:

**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

## FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGGCGGCGCTGCCCCTCCCCACACTCCCCCGCGAGAACGCTCGCTCG  
GCGCCCAAATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGGCTGTGGCGGCGACGCGAGCCCCGAGGAGGCCGCGCTGCCCGCGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCAATCAAGAACAGGTTTGAGTG  
GCCGCTCTTTGTGACCACTCTCCAGCATTTTTTCATGCAAAAGGATGGGATATCCGCCGT  
TATCGTGGCCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCAAACTATTTTCACAGTGACTCTTGGAATTT  
CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAGACAGCCCTTGATAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGCAACTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCCTGCCAGC  
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGTCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAAGGAGGCCATTCCCACTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAANTGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACTGAGAAGCCTTGACATCTTTCTTGTGTAAGTATTTAT  
TTTTGTCAAATTCAGGAAACATCAGGCACCAAGTGCATGAAAAATCTTTTCAAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTGAGGCTCT  
CCACACTCTTCACTATTATCTTGTGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTAGATAATCAGTAACCATAAACCCCTGAAGCTGT  
GACTGCCAAACTCTCAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGCTTGGCAGTACAAGGTAGT  
CTTGGAAGAAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCTGGGTCTTGAAC  
TACTTTAATAAATACTAAAAAACCACTTCTGATTTTCTTCAAGTGTGCTTTTGTGTAAAC  
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTTCATCTTCTGTAATC  
TTCCAAAGAAATATATCTTTGTAATCTCTCAATCTCAATCTACTGTAAAGTACCAGGGAG  
GCTAATTTCTTT

0970193-141504



## **FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSQCQQTDESEWFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG  
PGIFEDLQNYILEKKWQSVLEPLTGWKS PASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEBK  
DDSNEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTR  
EVEPEEAEEGISEQPCPADTEVVEDSLRQKSKHADKGL

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

# FIGURE 201

ATCTGGTTGAACTACTTAAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT  
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCACTCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAAATGGAATATCATCCTGATTTAGAAAAAT  
TTGGATGAAGATGGATATATCTCAATTACACTTCGACTCTCAAAGCAATACAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATTGGGGGTTCTTTCC  
AGCCCTTGTCTCCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTACAGCATGTCACT  
AAATTCCTGGGATGGAGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTTGGGATTTATAGTAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCTTTTCTCGGCCCCAGACTGAGGTACCATTGGCTCTGGGAGGATGGATCAACATT  
CTCTCTTAACCTTATTTAGATCAGAACCACAGCTACCCAGAAACCCATCTCCAAATTGTG  
TATGGATTACAGTGTCACTATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTGT  
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACGTGAATCTTAACCAAGAAATGAAGGGAGAGGCTGTGATTCTT  
GTATTTGTGCACCTACAGGTAGGCTAGTATTATTTTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAAGCTTGGATTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT  
CACTTTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTTGCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCGCTTGGCCTCCCAAAGTCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTTCAATCTGCCATTGACTTGGCATTACCTTGGGTAAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCTCAACTTCTAGCAGTATATCAGTTATGAATGAGGGTGAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCCTA  
CTTTTCTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCTTGGGTTCAAGCAATTCTCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACACACCCGGCTAATTTGTATTTTTTTAGT  
AGAGCAGGGTTTTCTCCATGTCGGTCAGGGTAGTCCCGAATCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCATGACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAACCTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTAATGTTTTTACAAATTTT  
ACCATTTTTTTTCAAGTAATTACTGTAATAATGGTATTATTGGAATGAACATATATTTCTCATG  
TGCTGATTGTCTTATTTTTTTTCACTTTCCCACTGGTGCTATTTTTTATTTTCCAATGGATA  
TTTCTGATTACTAGGGAGGCAATTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAAATGGATGATTTTATGTTATGTGGATTTTCAT  
TTCAATAAAAAAAACTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0970493.101501

## **FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912  
<subunit 1 of 1, 201 aa, 1 stop  
<MW: 22563, pI: 4.87, NX(S/T): 1  
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRFPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

# FIGURE 203

GGAGGGGAGGAGGAGCCACACAGGCACAGGCCGCTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA  
 CACAGGCTGGAGTCCAGTGGTGTGATCTTGGCTCATCTGAACCTCCACCTCCCGGGTTCAAGTGAATTTCTCATGCC  
 TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAGAGTAGTGAATCCCGTGGAGGAATATGACTTCCCAAG  
 TCCTCTCTGTCAGAGCAGCATGTTTCTGCTGAGTCTTGCTCTTCTGGTCCAAGTGCCACAGGCGAGGGGCCACAGG  
 GAAGACTTTTGGCTTCTGTCAGCCACGCGAACACAGACACACAGGAGCAGCTCTTCTCAACAAACCCACACAGAGCTTG  
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCAGAGTCCATGCCCCCTTTCTCTGACGCCACCTCTGTTCCCGA  
 TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCTCTGCTCACTTGGAGCCGATCTGCTGGAGATTACATCTTCTC  
 TATGGCAAGCTGACTTCTTGTCTGAGTGACAAGCCTTAGCTCTCTCTGCTTCCAGGACACAGGAGGAGGAGCTTG  
 GCTCAGGGCCCCCGGCTGTAGCCACTTCTGTCACTTCTGGTGGAGCCCTCAGAACATCAGCTGCCCACTGCC  
 GCGAGCTTCACTTCTCTCTTCCACAGTCTCTCCCAACAGCGGCCCTCAAAATGCTCTGGTGGACATGTGCGAGCTT  
 AAAAGGGACTCCAGCTGCTCAGCCAGTTCTTGAAGCATCCCCAGAAGGCTCAAGGAGGCCCTCGGCTGCCCTC  
 GCCAGCCAGCAGTGTGAGAGCCTGGATCGAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTCTCGAG  
 GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCAAGCCGCGCTCCAGGACCTGCATCATCCATCCCGG  
 CAGGAGGAGGAGCAGAGCAGATCATGGAGTACTCGGTGCTGCTGCCCTCGAACACTCTTCCAGAGGACGAAAGGC  
 CGGAGCGGGGAGGCTGAGAGAGACTCTCTCTGGTGGACTTCAGGACCAAGCCCTGTTCCAGGACAAGAAATTC  
 AGCCAAGTCTGGGTGAGAGAGTCTTGGGATTTGTGGTACAGAACACAAAGTAGGCAACCTCAGGAGCCCGGT  
 GTGCTCACTTTCAGCAGCAGTACAGCCGAGAAGTGTACTTCGAATGTGTGTTCTGGGTGAAGACCCCA  
 TTAGCAGCGCCGGGGACTTGGAGCAGTGTCTGGGTGTGAGACCGTCAGGAGAGAGAAACCAAACATCTCTGCTCTGC  
 AACCACTTGACTACTTTGCAAGTGTGATGGTCTCTCGGTGGGTGGAGCCCGGTGCAACAGCACTACTGAGC  
 CTCTCTCTTACCTGCGGTGTGTGTCTCTGCTCTGGCTGCTGCTTGTCAACATTTGCCGCTACTCTGCTCGAGG  
 GTGCCCCGCTGAGGAGGAACTCGGACTACACCTCAAGGTGCATGAACTCTGCTGCTGCGCTGCTTCTC  
 CTGCTGGACAGCAGCTCTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCAGTGCC  
 ATCTTCTGCACTCTCTCTGCTCTCCTGCTCTTCTGGATGGGCTCGAGGGTGAACACTCTACCACTCTGCTG  
 GTGAGGTTCTTGACCACTTCTCTCTCTGCTTACTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTT  
 CTGCTGACGCTTGTGGCCCTGGTGGATGTGGACAACATAGGCCCATCATCTGCTGTGTAGGACTCCAGAG  
 GCGCTCATCTACCTCTCCATGTCTGGATCCGGACTCTCTGCTGAGTACATCAACAACTGGGCTCTTCACTC  
 CTGCTGTTCTGTTTCAACATGGCATGCTAGCCACCATGGTGTGCAGATCTGCGCGCTGGCCCCACACCCAA  
 AAGTGTTCACATGTGCTGACATGCTGGGCCCTCAGCTGCTCTGGCTGGCTGGCTGATCTTCTCTCC  
 TTTGCTTCTGGCAGCTTCCAGCTTGTGCTCTCTTACCTTTTACGATCATCACTGCTTCCAGGACTTCTCATC  
 TTACTTCTGTACTGTGCTCATGCGGCTCAGGCCCGGGTGGCCCCCTCCCTCTGAGAGGCAACTCAGACAGCGCC  
 AGGCTCCCCATCAGCTCGGGCAGCACTCTGCTCAGCCGCTCTAGGCTCAGGCCCTGCTCCATCTCTGCTGGG  
 CAGAGATGGGCTCTGTCGACACTGCTCTGGGCCCGAGCCAGGCCCAAGCCAGGCTGACCGCAGACT  
 TTGGAAGGCCCAACGACCATGAGAGATGGGCCGTGGCATGGTGGAGCGACTCCCGGCTGGCTTTTGAATTG  
 GCTTTGGGGACTACTCGGCTCTCACTCAGCTCCCAGGGACTCAGAAGTGGCGGCCCATGCTGCTTAGGGTACTG  
 TCCCCATCTGTCCCAACCCAGCTGGAGGCTGGTCTCTCTTACAACCCCTGGGCCCGAGCCCTCATTGCTGGG  
 GGGCAGGCTTGGATCTTGAAGGCTCGGCACATCTTAACTCTGTCGCCCTGGCTGGGACAGAAATGTGGCTCCA  
 GTTGTCTCTCTCTGTTGCTCACTCTGAGGCACTCTGCTCATCTCTGTCACTTTAACTCAGGTGGCAACCAAGG  
 CGAATGGGCCCGAGGAGCACTTCAAGGCCAGAGCCCTGGCGAGGAGAGGCCCTTTGGCAGGAGCAGCAGCAGC  
 AGCTCGCTCACTCTGAGCCAGGCCCCCTCTCTCTCTCAGCCCCAGTCTCTCTCTCATCTTCTCTGGGGTCT  
 TCTCTCTCTCAGGAGCTGCTGCTGTCTGCTGTAAATGTTTGTCTACTGCAACAGCTCGGCTGCCCCTGAGCCA  
 GGCTCGGTACCGATGCTGGGCTGGGCTAGGTCTCTCTGCTCATCTGGGCTTTGTATGAGCTGCAATGGCCCTGTG  
 CTCACCTGACCAAGCAGCAGCTCTCAGAGGGGCCCTCAGCCTCTCTGAGGCCCTCTTGTGGCAAGAACTGTGGA  
 CCATGCACTCCGCTCTGTTTTCATCCCAACAGGACTGAGACTGACCTCTCTGTTGACACTGGCCCTA  
 GAGCTGACCTCTCTTAAAGAGTTCTCTCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCTGTT  
 TAATTCTGTCAACAAACACACACAGGGTGAATTTCTGCTGCTTGTAGGTGTAGGGACACAGATGACCGAGCT  
 GTCACTCTCTCTGCAACATCTCAGTCTGGTATGTGAGGCGTGGCTGAGCAGAACTCTCTGGAGCTACAGGACA  
 GGGAGCTCATCTTCTGCTTGGAACTCTGGAAGCTCTCTGAGGAGTCAAGGCTTGAATCTGACCTTGAATGAGAT  
 GGGAGAGATGTTCTTTTACGTACCAATCTTCTTGTCTTTTGAATATAAAGAGATGATGTTCTATTGTAGAGA  
 ATTTTGAAGCTGAGAGAGATCAAGAGAAAAATAAAAAATCAGCTGTTGTAATCGCTAGCAAAAAA  
 AA

0976193-101501

## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQTTLLFLLSLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTDLRISIENSE  
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLTFOHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRRE  
TOTSCFCNHLTYPAVLWSSVEVDVAVHKKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVLPC  
RRKPRDYTIKVHMNLLLAFLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLSVYITNLGLFSLVFLFNAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWWSMRLQARGGPSPLKSNDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

## **FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCTCTGCTG  
GACACGAGCTTCTCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCTGCACTTCTCTCTGCTCACCTGCCCTTCTCTGGATGGGCCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTCCTGTTCAACATGG

# FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTCGGTTCCAGGTCAGGTTTTCGCTTTGA  
 TCCTTTTCAAACCTGGAGACACAGAAAGGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGGAACTACCT  
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCTCGGCGGTGGTGAAGAGAGAC  
 TCGGGAGTCGCTGCTTCCAAAGTCCCCCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTTCGGGC  
 TTCTCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGCGGAATCCAACTGAGTAGTAAATTC  
 AGTTTTTCAGCAACCAAGGAACAGAAAGCGGATACAAGATCTCAGCATGAGAGAAATTTACTGTGTCTACTAATG  
 GAAGTATTCACAGCCCAAGTTTCTCTACTATTCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
 AGGAAATGTATGGATTACAATCTACGTTTGTATGAAAGATTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
 ATGATTTTGTAGAAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCA  
 GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGTAGTAATATTTCTCTGAACAGGGT  
 TCTGCATCCACTACAACATTGTGATGCCACAATTCAAGAAGCTGTGAGTCCTCAGTGCTACCCCTTTCAGCTT  
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGAACCTTATTCGATATCTTGAAACC  
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTTTTGTTTTGGAA  
 GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT  
 CAGTGTCCATAAGGGAGAAGCTAAAGAGAACCGATAOCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG  
 GTGGGAACCTGTGCTGTTGTCTCCACAATGTCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACC  
 ACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGACGGGATTGCAAAATCACTCACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGACTGTGTGTGACAGGGAGCACAGGAGGATAGCCGATCACCACAGCAGCTCTTGCCCA  
 GAGCTGTGACGTGACGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCT  
 TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCAATTCTGAAGAGGAGACATCAACAGAATTAGGAGTTGTGCA  
 ACAGCTCTTTTGAAGAGGAGGCTTAAAGGACAGGAGAAAAGGTTCTCAATCGTGGAAAGAAAATTAATTTGTAT  
 TAAATAGATACCCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTACTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
 GATAACGCTTACGGGTAATGTTCAGTACAGGAAAAAACTGTGCAAGTGAGCACTGATTCGCTGGCTTGCCTTTC  
 TCTAAAGCTCCATCTCTCGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT  
 ATGTAAACAGAACTCTATGTCTACAACTCGTTTAAAGGAACATGTTGCTATGAATTAACCTTGT  
 GTCATGCTGATAGGACAGACTGGATTTTTCATATTCTTATTAATTAATTTCTGCAATTTAGAAAGAGAACTACA  
 TTCATGGTTTGAAGAGATAAAGCTGAAAGAGAGAGTGGCTTATCTTCACTTATTCGATTAAGTCAGTTTATTTG  
 TTTCAATGTGTACATTTTTATATTCTCTTTTGACATTATAACTGTGGCTTTTCTAATCTTGTATAATATATCT  
 ATTTTTACCAAAGTATTTAATATCTTTTTTATGACAACTTAGATCACTATTTTTAGCTTGGTAAATTTTTCT  
 AAACACAATTTGTATAGCCAGAGGAAACAAAGATGATATAAATATTGTGTCTGACAAAAATACATGTATTCCA  
 TTCTCGATGTGGTCTAGAGTTAGATTAACTGCAATTTAAAAAACTGAATTGGATAGAATTGGTAAGTTGCAAA  
 GACTTTTTGAAAAATTAATTAATATCATATCTTCCATCTGTATTGGAGATGAAAATGAAGCACTTATGA  
 AAGTAGACATTAGATCCAGCCATTCTAACCTATCTCTTTTGGGAAATCTGAGCTAGCTCAGAAAAACAT  
 AAAGCACTTTGAAAAAGACTTGGCAGCTTCTGTATAAAGCGTGTGTGCTGTGAGTAGGAACACATCTCTATTTA  
 TTGTGATGTTGTGGTTTTATATCTTAACTCTGTTCCATACACTTGTATATAATACATGGATATTTTTATGTACA  
 GAAGTATGTCCTTAACAGTTCACTTATGTACTCTGGCAATTTAAAGAAAATCAGTAAAAATTTTTGCTGT  
 AAAATGCTTAAATATNGTCTAGGTTATGTGTGACTATTGGAATCAAAATGATTGAATCATCAATAAAAAG  
 ATGTGCGCTATTTGGGAGAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGATACACAGGTTATCGCGC

0073493.101501

## FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

### **Signal sequence:**

amino acids 1-14

007513-13004



# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTGCTCTCTTCAACGAGACCTCTACATTCATTTTGAAGA  
 AGACTAAAATGSGTGTTCCTAATGTGGACACTGAAGAGACAAATCTCTTATCTCTTTTAAACATAATCTCTAATTTCC  
 AAACCTCCTTGGGGCTAGATGGTTTCTTAAACCTCTGCCCTGTGATGTCACCTCTGATGTTTCCAAAGAACCATGTG  
 ATCGTGGACTGCACAGACAGCATTTTGAAGAAATCTCTGGAGGTATTCACAGAACACACAGAACCTCACCCCTC  
 ACCATTAAACCACATACCAGATCTCTCCAGCGCTCTTTTACAGACAGTGGACCATCTGGTAGAGATCGATTTCAGAA  
 TGCACCTGTGATCTATTCCACTGGGGTCAAAAACACATGTGTCATCAAGAGGCTCGAGATTAAACCCAGAAAC  
 TTTAGTGGACTCATTATTAAAAATCCCTTTACTGGATGGAACACAGCTACTAGAGATACCGAGGGCCCTCCG  
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGATCTAACAGAACTGGCC  
 AACATAGAAATACTCTACTCTGGGCCAAAACCTGTATTATCGAAATCCTTGTATTGTGTTTCAATTTCAATAGAGAAA  
 GATGCCCTCTCTAAATCTGACAAAATTTAAAGATGCTCTCCCTGAAAGATAACATGTACAGCCGCTCCCTACTGTT  
 TTGCCATCTACTTTTAAACAGAACTATATCTCTACAAACACATGATTGCAAAAATCCAAAGAGATGATTTTAATAAC  
 CTCAACCAATTACAAATCTTGACCTAAGTGGAAATGGCCCTCGTTGTATAATGCCCATTTTCTTTGTGGGCGG  
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTGATGCGCTGACAGAAATTTAAAGTTTACGCTCA  
 CACAGTAATCTCTTTCAGCATGTGCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
 CAAAACCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCAATTTCTCCCCAGCCTCATCCAATTGGATCTG  
 TCTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCAACAGCATTTTCTTCACTGAAAAGCCCTG  
 AAAATCTGCGGATCAGAGGATATGTCTTAAAGAGTTGAAAAGCTTAAACCTCTGCCATTACATAATCTTCAA  
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAATTTGCTAACCTCAGCATGTTTAAACAAATTTAAAGA  
 CTGAAAGTCATAGATCTTTTCAGTGAATAAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTCTGCTCAAA  
 CGCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTTGAACAAATACATTTTTCAGATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTCTTTTCATGCTGTGTTAATGAAAGCTGCTACAAGTATGGGCGAGCC  
 TTGGATCTAAGTAAAAATGATATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTCTTCTTCTCAAAATGCCCTG  
 AATCTGTCAAGAAATCTGATTGACCAAACTCTTAATGGCAGTGAATCCAACTTTAGCAGAGCTGAGATATTTG  
 GACTCTTCCAACAACCGGCTGATTACTCCATTCACAGCATTTGAAGAGCTTCAACAACTGGAAGTTCTGGAT  
 ATAAAGCAATAGTACCTTATTTTCAATCAGAAGGAATTTACTATATGCTAACTTTTCAAGAACTCTAAAGGTT  
 CTGCAGAACTGATGATGAACGACATGACATCTCTCTCCACAGCAGGACAGTGGAGAGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGGAATCACTTAGATGTTTATGGAGAGAGGTTGATAACAGATATTTACAATTTTCAAG  
 AATCTCTTAAATTAGAGGAATTAGACATCTCTAAAAATTCCTTAAGTTCTTGGCTCTGGAGTTTGTGATGGT  
 ATGCCCTCCAAATCTAAAGAAATCTCTCTTGGCCAAAATGGGCTGACCACTGTCCCTGAGAGATTATCCAACTGTTC  
 CTAAGAACCTTGGAACTTTGGACCTCAGCCACACCACTGACCAAGTATTTTACAAAGATGCCTTC  
 AGAAGCCTCAAGATCTGATCTTAAAGAAATCAAAATCAGGAGCTGACGAAGTATTTTACAAAGATGCCTTC  
 CAGTTGCGATATCTGGATCTCAGCTCAAAATAAAATCCAGATGATCCAAAGACGACGTTCCAGAAATGTCTTC  
 AACATCTGAAGATGTTGCTTTTGTCATATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGCTGTGCTGGG  
 GTTAAACCATACGGAGGTGACTATCTTACCTGGCCACAGATGTGACTTGTGTGGGCGCAGGAGCACACAGGGC  
 CAAAGTGTGATCTCCCTGGATCTGACACCTGTGAGTTAGATCTGACTAACCTGATTTCTCTCACTTTCCATA  
 TCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCACTCTATTCTGGGATGTGGGTATATTACCAT  
 TTCTGTAAGGCCAAGATTAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTATTGTGTAT  
 GACACTAAAGACAGACTGTGACGAGTGGGTTTGGCTGAGCTGGGCCAACTGGGAAGCCCAAGAGAGAAA  
 CATTTTAAATTTATGTCTCGAGGAAGGGACGTGTTACAGGGCAGCCAGTTCTGGAANAACCTTTCCAGAGCATA  
 CAGCTTAGCAAAAAGACAGTGTTTTGTGTGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATGACATTTTAC  
 TGTCCCACTAGAGGCTCATGTGATGAAAAGTTGATGTGATTATCTGATATTTCTTGAGAGCCCTTTCAAGAG  
 TCCAGTTCTCCAGCTCCGGAAGGCTCTGTGGGAGTTCTGTCTGTGAGTGGCCACAAACCCGCAAGCTCAC  
 CCACTCTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGGCTATGTCAGGTGTCTCAAGGAA  
 ACGSTCAGCCCTTTGGCAAAACACAACTGCCTAGTTTACAAGGAGAGCTGGC

09/7/81 13.101501

## FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFFKTLPCDVTLDVPKNHVIDCTDKHLTEIPGG  
IPTNTTNTLTINHIPDISPASFHRLDHLVEIDFRCNCVFIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYR  
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQEBDLSONFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKLMNDNDISSSTSRIMESES  
LRTLFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSCLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVWNHTEVTIP  
YLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPATEWVLAEVLAKLEDPREKHFNLCLLE  
RDWLPGQPVLLENLSQSISQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWFTNPQAHPHYFWQCLKNALATDNHVAYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

# FIGURE 210

GGGTACCAATCTGCGCGTGTCTGCAAGTTACGGGAATGAAAAATTAGAACAACAGAAACATGGAAAAACATGTTCTCTC  
 AGTCGTCAATGCTGACCTGCAATTTTCTGCTAATAATCTGGTTCTCTGTAGTTATGCGCGGAAGAAAAATTTTCTTA  
 GAAGCTATCTCTGTGATGAGAAAAAGCAAAATGACATGCTATTTGCAAGATGTGCGCAATCTGCTGACATACAGGAAG  
 TTCCCAAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGTAATTTTCACTACACACNTAAGAAATGAAT  
 CATTTTCAAGGGCTGCAAAATCTCATAAAATAAATCTAAACCAACACCCCAATGTACAGCACAGAACGGAATCT  
 CCGGTATACAAATCAATGGCTGTGAATATACAGACGCGGGCATTTCCCAACTTAAAAACCTAAGCGGAGTATCTGTC  
 TTGAAGACAACAGATTACCCCAATACCTCTGGTTTGGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA  
 ATATATACAACAATACTAAGAGGGGCATTTCAAGACTTATAAATCTGAAAAATCTCTATTGGGCTGGAACTGCT  
 ATTTTAAACAAAGTTTGGCAGAAAACTTAACATAGAAGATGGAGTATTGAAACGCTGACAAAATTTGGAGTTGCTAT  
 CACTATCTTTCAATTTCTCTTTCACACGTGCCACCCAACTGCCAAGCTCCCTACGCGAAATCTTTTCTGAGCAACA  
 CCCAGATCAAAATACATTAGTGAAGAAGATTTCAAGGGATGTATAAATTTAACTATACATAGATTAAAGCGGAACT  
 GTCCGAGGTGCTTCAATGCCCACTTTCCATGCGTGCCTTTGTATGGTGTGCTTCAATTAATATAGATCGTTTGT  
 CTTTTCAAACTTGACCCAATCTCGATACCTTAAACCTCTCTAGCACTCCCTCAGGAAGATTAAATGCTGCTGTGT  
 TTAAAAATATGCTCATCTGAAGGTGCTGGATCTTGAATTTCAACTATTAGTGGGAGAAATAGTCTCTGGGGCAT  
 TTTTAAACGATGCTGCCCGCTTAGAAAACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCAT  
 TTAATATTTCCAGAACTTTCTAAACTTTTGTCTCTACGGGCATTTGATTTAAGAGTTATGTGTTCCAGGAAT  
 TCAGAGAAGATGATTTCCAGCCCTGATGCAGCTTCCAACTTATCGACTCACTGGGTATTAATTTTAACTA  
 AGCAATCGATTTTCAAACTTTCCAAATTTCTCCAATCTGGAATTTATTTACTTGTGAGAAACAGAAATACCA  
 COTGGTGGTAAAAGATACCCGCGAGAGTTATGCAAAATGTTCTCTTTCAAGCTATATCCGGAAACGACGCTCAA  
 CAGATTTTGAAGTTGACCCCACTTGAACTTTTATCTTTTCAACCGTCTTTTAAAGCCCAATGTGCTGCTCT  
 ATGGAAGAGCTTAGATTAAAGCTCAACAGTATTTTCTTATTGGGCGCAACCAATTTGAAAATCTTCTGACGA  
 TTGCTGTGTTAAATCTGTCTGCAAAATGCAAGTCTCAAGTGTAAAGTGAAGTGAATTTTCAAGCTCTGCTGAT  
 TCAAATATTTGGAATTTGACAAAAATAGACTAGACTTTGATAATGTTAGTGTCTTACTGAAATTTGCGAGTTGG  
 AAGTTCTAGATCTCAGCTAATAATACACTATTTTCAAGATACAGCGGTAACACTCATCTAGAATTTTATCAAA  
 ATTTTCAAAATCTTAAAGTTTAAAACTTGAGCCACAACAACTTTATCTTTAACAGATAAGATAAATCTGGAAA  
 CGAAGTCCCGTGGAGAAATAGTTTTTCAAGTGGCAATCGCTTGCATATTTTGTGAATGATGACCAACAGGTATA  
 TCTCCATTTTCAAGAGTCTCAGAAATCTGACAGCTCTGGAATTTATCCCTTATAAGGCTGAAGCAACTCCAAATG  
 AAGCATTTCTTAATTTGCGCGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGGA  
 CATTAATCTCCAGAGTTTCTCGTCTCGAGTTGCTGTGACTTACGTGGAACCAAACTCTCTTTTAACTGATAGCT  
 TATCTGACTTTTACATCTTCCCTTGGGACACTGCTGCTGAGTCTATAACAGAGATTTCCCACTCCCTCTGGCTTTT  
 TTTCTGAAGTCAGTAGTCTGAAGCACTCGATTTAAGTTCCAATCTGCTGAAACCCCTTTGAATGCACCTGTGCAATTTGAG  
 AAACATAAGACCAACCAAAATTTATCTATGTTGGAACATACAGGAAACCCCTTTGAATGCACCTGTGCAATTTGAG  
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCAGACTGCTAGATGTCAATTTGTGCCAGTCTG  
 GGGATCAAGAGGGGAAGATATTGTGAGTCTGGAGCTAAACAATTTGTGTTTCAAGTGTCTGCTCAGTGAATTTAT  
 TTTTCTTCAAGTCTCTTATACCAACCATGTTATGTTGGCTGCCCTGGCTCACCATTGTTTATCTGGAATGTT  
 GGTTTATATATAATCTTTTGTAGCTTAAAGGCTACAGGCTCTCTTCCATCTCCAAATCTTTCTATGATG  
 CTTCATCTTTCTATGACCAAAAGATGCTCTGTACTGACTGGGTGATAAATGAGCTGCGCTACCACTTTGAAG  
 AGAGCCGAGCAAAACCTTCTCTTTGCTAGAGGAGAGGGATTTGGGACCCGGGATTTGGCCATCATCGACAACCT  
 TCACTGAGAGCATCAACCAAGGACAGAAAAACAGTATTTGTTTAAACAAAAAATATGCAAAAGCTGGAAATCTTA  
 AAACAGCTTTTATCTTGGCTTTTGCAGAGGCTAATGGATGAGAACATGGATGTATTATTTATCTCTGCTGGAC  
 CAGTGTATACAGCATTTCTAGATTTTGAGGCTACGCGAGCGGATCTGTAAGAGCTCCATCTCTCAGTGGCTTGACA  
 ACCGGAAGGCGAGAAGCTGTGTTTGGCAAACTCTGAGAAATGTGCTGTGACTGAAATGATTCAGGTTATACCA  
 ATATGTATGTCGATTTCCATTAAGCAATATCACTGACGTTAAGTCATGATTTTCCGCGCATATAAAGATGCAAG  
 GAATGACATTTCTGTATAGTTATCTATTTGCTATGAACAAATTTATCCCAAACTTAGTGGTTTAAACCAACCA  
 TTTTGTCTGGCCCACTTTTCAAGGGGTCAGGAGTCTCAGGCTCAGCATAACTGGGTCTCTGCTCAGGTTGCTCAG  
 AGGCTGCAATGTAGGTTTTCAGGAGACATAGGCATCACTGGGCTCACTCATGTGGTTGTTTCTGATTTCA  
 ATTCTCTCTGGGCTATTTGGCCAAAGGCTATATCTCATGTAAGCCATGCGAGGCTCTCCCAACAGGCAAGCTTGCTT  
 ATCAGAGTCAACAAAAAGAGAGGTTGTGTAGCAAGATGAAGTCACAATCTTTTGAATTCGAATCAAAAGATGAT  
 ATCTCATCACTTTGGCCATATTTCTTTTGTAGAAGTAAACACAGGTCACAGCTCTCATGGAGTGAACCTT  
 TCACTGCGAGAAACAGCTGGAACCAAGATGTTGAGTCTGATTGCTTCAAGTGTGATGAGTCAATTTTCTCT  
 TGACTGCTGCTGGATGGCCGCTCATCTTGTATGATAGATTGTGAATATCAGGAGGCAAGGATCACTGTGGGACC  
 ATCTTCAAGTGTGATGACCACTCTCTTTTCAATATCAAGAACTTCAAGGTTTGAAGTCAATTTGAGTCTGATTA  
 TTAAGCTGTGTTTATATTTATCATATCTATGGCTCATCGTTTATATTTGCTGTGGTTTGGCTCGGTTTAT  
 TTAAGTCTTTTAAAGCATCTTTTATCTCTTACCAATTTTAAAGATGTCAGCTAAATTCGAAGCTTTTGGTCTATA  
 TTGTTAATGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCAATTTTCAAAAAA

## **FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLENTQIKYISEEDFKGLINL  
TLDDLSGMCPRCFNAPFCVPCDGGASINIDRFAPQNLTLQRLYNLSSTSLRKINAAWFKNM  
PHLKVLDFEFNVLVGEIVSGAFLTMLPRLEILDLSFNLIKSGSYPOHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQPLNLSTINLGINFIKQIDFKLFQNFNSLEIIYLSNRIISPLV  
KDTRQSYANSSSFQRHIRKRRSTDDEFDPHSNFYHFTTRPLIKPQCAAYGKALDLSNLSIFFI  
GPNQFENLPDIACLNLANSNAQVLSGTEFSAPHVKYLDLTNNRLDFDNASALTELSDELEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT  
LLQQFPRLLELLDLRGNKLLFLTDLSLDFTSRLTLNLSHNRISHLPSGFLSEVSSLKHLDL  
SNLLKTINKSALETKTTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGFLFWQTLRNVVLTENDSRYNMYVDSIKQY

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 826-848

0076193.104501

## FIGURE 212

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGTGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGCCTGCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCTGGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCCGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGTGCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCGAGCCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGTGGAGGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCATGAAGGAA  
GAAGTGACAGAGGTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCCTCC  
TGGTGCACCTCCTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG  
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGAACTGCCACGCGCCCCAGGCTG  
GACTGAGCCCCTCACGCGCCCTGCAGCCCCATGCCCTGCCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTCTCCTCCTCCC  
TTCCTCGGGAGGCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCCCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCTCAGTGGGGGCTGCTGCCCTGACCCCCAGCACAAATAAAATGAAACGTGA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCGCCATGGCCCAACTGTGTTATTCAGCTTATAATGGTTACAAAT

Figure 1. The structure of the proposed model.

**Signal sequence:**

1-19

## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCCTGGGTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCTGCTTGGCTGGGCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGCCCGGGGAGGGGAATGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGCCCTGTCCGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTTCG  
TGCAGCGTGTGTACAGCCCTTCTCACCACCTGCGACGGGCACCGGGCTGCAGACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGACGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGTGCCCCCGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCAGTGTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGAGGGCCCCCAGGGTGGCCCCAACC  
ACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGTGCTGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGACGCTCCTGGTGCACTCCTTCAGCAGCTCGGCCGATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTCGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGA  
CTCGTGACTGCCACGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCTGCAGCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCTCCTCTTCTCCTCCCCCTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGTGGGATCTTCTGTGAATCCACCCTGGCTACCCCCACCTGGCTACCCCAACGGCA  
TCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGAC  
CCCCAGCACAATAAAATGAAACGTG

007393-10501

## **FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTCCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSSEQISFLEEQLGSCSCKDS

**Signal sequence:**

1-19

00703-1000



**DECEMBER**

CCACACGCTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCCTC CAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGTC  
CCCTGTCCGGGGGATGACTGATTCTCTCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCG  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGTTGTGGC  
AGTGGGCGGCACAGAGCAGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCAG  
GGGACCTGTCTCCGAGTCTGTTCTGTGCAGCGTGTGTACCAGCCCTTCTTACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGACGCCCTGG  
GCTGGCCCCTGCCAGGCCTCGTACGCGTCTGCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG  
CCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGTGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC  
TTCCAGCAGCTCGGCCGATCGACTCTCTGAGCGAGCAGATTTCTTCTTGAGGAGCAGCT  
GGGGTCTCTGCTCTGCAAGAAAGACTCTGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAAATGCTGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCTTCTCTGGGAG  
GCTCCCCAGACCTTGGCATGGGATGGGCTGGGATCTTCTCTGTAATCCACCCCTGGCTACC  
CCACCTCTGGCTACCCCAACGGCATCCCAAGGCACAGGTGGGCCCTCTAGCTGAGGGAAGGTAC  
GAGTCTCTCTGCTGGAGCCTGGGACCCATAGGCACAGGCGAGGCAGCCCGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAATGAAACGTG

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLADGTL CVPKGGPFRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKDS

**Signal sequence:**

1-19

0978193-102501

# FIGURE 218

GGTGGCCACAGCTGGTTTAGGGCCCCGACCAGCTGGGGCCCCTTGTACAGGAGAGACAGCCTCCCCGGCCCCGGGAG  
 GCAAGTGCCTGCCACCTTTGGCTGCCAGCTGATTCCTGGGACGGTCCGTTTCTGCGCTCAGCTGCCGGCCG  
 AGTTGGGTCTCCTGTGTTTACGGCCGGCTCCCCCTTCTCGGTCTCCCTTCTCCCGCTGGGCGGGTTATTCGGGAGG  
 AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCGAGGAATAGCAGGCAAGTGAT  
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTCTCGTGTAATCGCAAAACCATTTTGGAGCAGGAATTCGAATCA  
 TGCTGTGATGGTGGTGAGAAAGAGGTGACACGAAATGGGAGAACTCCCAGGCAGGAAACACCTTTTGCTGTG  
 ATGGCCGGCTCATGATGGCCCCGCAAAAGGGCATTTTCTACCTGACCCCTTTCTCATCTCTGGGACATGTACAC  
 TCTTCTTCCGCTTTGAGTGCCGCTACCTGGCTGTTCAGCTGTCTCCTGCCATCCCTGTATTGTCTGCCATGCTCT  
 TCCTTTTCTCCATGGCTACACTGTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCCGGGCGCTACCAGATG  
 AAGCAGCTTTATAGAAATGAGATAGAGCTACCAATGGTGGGTGCCCGAGGGCCAGCGACACCGCCCTCGTA  
 TCAAGAATTTCCAGATAAAACCAACGATTGTGAAACTGAAATACCTGTTACACATGCAAGATCTTCCGGCCCTCCCC  
 GGGCCTCCCATTTGACGATCTGTGACAACTGTGTGAGGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG  
 TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCCCTCCTCAATCTATGCTTCGCT  
 TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAAATGGCTCTTGGAGACATTGAAAGAAACTCTCGGAACGT  
 TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTCTGGGACTGACTGGATTTCATACTTTCTCGTGG  
 CTCTCAACCAGACAACCAATGAAGACATCAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTCTGTGTGGCCCCCTGCCCCAGTGCTGGATCGAAGGGGTA  
 TTTTGCCACTGGAGAAAGTGAAGTGCAGCTCCCACTCAAGAGACCAGTAGCAGCTCTTGCCACAGAGCC  
 CAGCCCCCAGACAACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCTCCCGAAGAGATGCCACCTCCAG  
 AGCCCCCAGAGCCACCAGAGAGGCGAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGCTTTTGTGTGTGTT  
 TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTAACT  
 GTTTTCTTTGGCTTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTAAATTTCTGAACT  
 CAAGGCTGGGCAAGATGTCACTCACTCTGATAACTGGAATAAGGGTCTCTTGGGCCCTGGCACTGGTTCT  
 CCATGGCTCAGCCACAGGGTCCCCCTTGGACCCCTCTCTCCCTCAGATCCAGCCCTCTCGTCTGGGTGAC  
 TGGTCTCATTTCTGGGCTAAAAGTTTTGAGACTGGCTCAAACTCTCCAAAGCTCTGCACTGCTGAGTCCAGA  
 GGCAGTCAAGAGACCTCTGCCAGGGGATCTTAAGTGGTCTTTCAGAGTGAAGAGAGAGGAGAG  
 TGGGTCAGAGATTCTCCTGGCCACAGGTGCCAGCAITGCCCAAACTCTTTAGGAATGGGACAGTACT  
 TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTCTCTTTGACTCTGCTCCATTAGAG  
 CAGGAATGGCAGTAATAAAGTCTGCACTTTGGTCATTTCCTTCTCAGAGGAAGCCCGAGTGCTCACTAAAC  
 ACTATCCCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCAAGAGAG  
 GCTCTCCTCTCTCTCTCTCCCCCGATGACCTCAAAAAAAAAAAATGCTAACAGTTCTTCCATTAGCCCT  
 CGGCTGAGTGAGGGAAGGCCAGCACTGCTGCCCTCTCGGGTAACCTACCCCTAAGGCCCTCGGCCCACTCTGGCT  
 ATGGTAACCACTGGGGGCTTCTCCAGCCCCGCTCTTCAGCACTCTCACCGGAGAGTCCCAAGGCCACTT  
 CACCCTGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT  
 ATTATATGTGGCTATATTTCTAGAGCACTGTGTTTCTCTTTCTAAGCCAGGGTCCGTCTGGATGACTTAT  
 GCGGTGGGGGATGATAAACCGAGCTTTTCATCTATTGGAAGGCCATTAACTGTGCTAATGCA

0070707.10.50.01

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV  
QLSPAIPVF AAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL  
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLCFFTLWSVVGLTGFHTF  
LVALNQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLEPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPQEAAEA EK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

057073-10504

## **FIGURE 220**

AAAACCCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAACTCTATGTCTTCGCCTCA  
ACATCGT

0978193.101511

## FIGURE 221

0076437-10504

GTGTGTCTCTTCAGCAAAACAGTGGATTAAATCTCCTTGCAACAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAAGAAAGAAAGAA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCATATT  
GACAACCGGGTACC CGGGTGGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA  
CAAGTGGTGCTTGGATCCTCGCGTGGTCCTTCTGAGCAACCCAAACGCAGTACAGCATCG  
AGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATT CAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATATCCACCATA  
TTTCAGAAGCCAAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAAACAGACCTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACACACTTGCCTGGCCTCCAACAAGCTGGGCCACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGT CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATTGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCGCCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAACTCTTGGGGGAAAAGAGTTTAAAAAAGAAATTGAA  
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTCCCAACCGGGAAGAACACAGC  
ACACCCGGCTTGAGACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTC AATCAGTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACCTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## **FIGURE 222**

MKTIQPKMHNSISWAIFTGLAALCLFQGVVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQXSIEIQNVVDVYDEGPYTCVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVVRVVKVTVNYPPYISEAKGTGVPVGQKGTLCCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Signal peptide:**

amino acids 1-28

007313-10564

050307

GAAAAAAATCATGAAACCATTCCAGCCAAAAATGCACAATTCATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCAGCGGAGATGCCACCTT  
CCCCAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCACTA  
TTGACAACCCGGGTCAACCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAAT  
GACAAGTGTGCTCGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG



# FIGURE 224

ATGGCTGGTGACGGCAGGGGCGGGGACCGGGGCCGGCGGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCTGGCCCCGACTCCACCAATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAAGACAGCTGTTAGGCTCAGCAGCGCAGCTGGAGCTGGTCTTACGAGGTGCCTCTCTACTGCTGGCT  
GCCTGCTCTCTGGGCTGCTTGGGGCCCTAGGGGTCAGTACCAAGAGACCCATCCCAAGCAGCCTTGCCTTACA  
GAGGGCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTTCGAGGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGA AAAACACCACTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACTATCTTGGCTACAGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA  
GACCTCATTTGAGAAGATTGGTGGTGGAACTTACGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAG  
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAACGCTCTACATCAGTGGCAGCTTAAGAGTTTCAACAGC  
AATGTTATCCAGGTGGACAGCTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCATCTGGAATTACATGGAGGAACCTGGGATGCTGCTGGGTGGGCGGCCCACTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACTCAGAGTGGCCAGGACAGGGCGCGAC  
GAGGAGAGATCTACACAAGATGAGCATTTCGGAGCTCGAGGCTTGGCGCCCTCCATGGACTGGCTTGAAGTTC  
CTGTCTTTCTTGCTGTACCAATTGGAGTTGAGTGACTCTGAGCCTTGGTGGTGTATGGGATGGATTATTTCAG  
CAGGTGTGAGAGCTCATCAACCGCAGCGAACCAAGCATCTGAAACAATTACCTGATCTGGAACTGGTGCAAAAG  
ACAACTCTAGCCCTGGACCGAGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCTCTATGGCACTAAGAAG  
TCTCTGTGTCCGAGGTGGCGAGACCTGCATCTCCAACCGATGACGCCCTTGGCTTTGGCTTTGGGGTCACTCTTC  
GTGAGGCCACGTTTTCAGCCGAAAGCAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATCTGAG  
GAGCGCTGGGACAGCTGGTTTGGATGGATGAGAGACCCGCGAGGCGAGCAAGGAGAAAGCAGATGCCATCTAT  
GATATGCTTGGTGTTCAGCACTTTATCTCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAACATGTGAATTGTGACAACTTCTCTGCAAGGTTTATGGCTGACCACTCCGCAAG  
CTTCCAGCCGAGACAGTGGAGCATGACCCCCAGACAGTGAATGCCACTACTCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCTCTGAGGCCCTCTTATGCCCGCAACCAACCCAGGCCCTGAACTCTGGTGGCATC  
GGTGTGGTCATGGGCCATGAGTTGACGCATGCTTTGATGACCAAGGGCGGAGTATGAGCAAGAGAGGAACTG  
CGGCCCTGGTGGCAGAAATGAGTCCCTGSCAGCTTCCGGAACCAACAGCGCTGCATGGAGAAACAGTACAATCAA  
TACAGGTCAATGGGAGAGGCTCAACCGCCCGCAGACGCTGGGGAGAGCAGCACTGCCAGCCGTGGGGCTCACC  
GCTGCCATCAATGCTTACAAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCACTGCCAGCCGTGGGGCTCACC  
AACCAACAGCTCTTCTCTGGTGGGATTGCCCCAGGTGTGGTGTCTCGTCCGACACACAGAGAGCTCTCACAGGGG  
CTGGTGACCGACCCCAACAGCCCTGCCCCCTTCCGCTGCTGGGCACTCTCTCCAACCTCCCTGACTCTCTGGG  
CACTCTGGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACTGGGGCAGCTCTCTGACAAAGCTGTTTGTCTCTGGGTGGGAGAGCAAC  
ATGCAAGCTGGGCTGGGCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGACCTCTCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCTGCCCTCAGCAGAGGCCCAACCATTCCTGTGACATCTTTCGTGTCAACCT  
GCCTGGAAGAGGTCTGGGTGGGAGGCGAGTTCCCATAGGAAGAGTCTGCC

0070403-10159

## FIGURE 225

MNVALQELGAGSNVGFQKGTQRQLLSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH  
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA  
ILKHLENTTPNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNR TAN EKVL TAY  
LDYMEELGMLLGGRPTSTREQMQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLLESDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSK EIAEGMI  
SEIRTAFEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISED SF  
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELT HAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

0978193.101501



## FIGURE 227

GGCCGAGCGGGGTGCTGCGCGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGCCCGGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACC GCCTGGCCCGAC  
TCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGCTGGATTTCGGA  
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATCTTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACTAGTGAACAACTGCCCT  
CCTTCTTTCTCTCTTTCTCTCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTTCC  
TCTTATTTCTTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTGAGGATTACAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTCTGAAGAGATTGCATTTGAGCCAGGTCTGTAG

097893-101501  
10510-66866

## **FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCGCAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCTTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAAGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAAACGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGGC  
ACTTCGGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACA  
GGTGACATGAGTACAGACCTCCTCAATCAACACATGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCACCATTCAGTGTGACATCTTCCGTGTCAACCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCTGCCGTGCCTGCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCAGGCTCACTCAGTGCACACTAGGGGTGGACTCAGCTCTGTCT  
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGTCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCTGGGCTGAGAGGGGAAGTGACATATGTGTAGCGGGTACTGGTTCTCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGTTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

0978193-101504

# FIGURE 229

CCCACGCGTCCGAGCGCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCAAAAACACCCGAAAAACAAAAGAGAGAAAACACCCCAACTGGGGTGG  
 GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCAAAAAAGAAAAAAGAAAAA  
 AAAAAAAGAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCAGCAGGGGG  
 TGGGGAGTGCAGCTGAAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGACAGGGTGCTTGTGTGCTCGAACCAGTGGCTGGCGGGCGTGCTCCTCAGCCTGTG  
 CTGCTGCTACCCCTCCTGCTCCTCGGCTGGACAGAGTGTGGACTTCCCTGGGCGCCGCTGG  
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAGATGGAGCT  
 TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTTTGGCGGAGGTGATAGTGGTCACT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGACTACAGCCTCCAGATACAGAAATG  
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTCCAGACTCAACATACACCCAGAACA  
 ATGCAGGTGCATCTAAGTGTGAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAACCCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCCCTCAGCAAAACCACTTTGAAAATGGACAATATTTGGACATT  
 TATGGAATTACAAGGGACCAAGGCTGGGGAATATGAATGCAGTGCAGGAAAATGCTGTGTCAAT  
 CCGACATGGTGAGGAAGTAAAGTTGTTGTCACTTTGCTCCTACTATTGAGAAATTAAT  
 CTGGCACCGTGACCCCGGACGCGAGTGGCTGATAAGATGTGAAGGTGCAGGTGTGCGCGCT  
 CCAGCCTTTGAATGGTACAAGGGAGAGAAGCTCTTCAATGGCCAAAGGAATTATTAT  
 TCAAAATTTTAGCACAAGATCCATTCTCACTGTTACCAACGTGACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAAACAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCCT  
 CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCCTGCTGTGATCCT  
 TGTGTTGACACTGCTCCTCTTCCACGACATATTCTACTGAAGAATGCCATTCTACAAATAA  
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCATGGCTGGATCCAACT  
 GGTACAGTTTGTAAAAAGCAGCGTGGGATATAATCAGCAGTCTTACATGGGGATGATGCC  
 TTCTGTAGAATTGCTCATTATGTAATACTTTAATTCTACTCTTTTGTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCTTTTAAAGACGTGAAAGCTCTGAAATTAATCTTTTAG  
 AGGATATTAATTGTGATTTTCATGTTTGAATCTACAACCTTTCAAAGCATTTCAGTCATGCT  
 CTGCTAGGTTCAGGCTGTAGTTTACAAAAACGAATATGTCAGTGAATATGTGATCTTTAA  
 GGCTGCAATACAAGCATTCACTGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAGATG  
 CATTTTTTTCTTTTGTATAAAAAAGCAAAATATATTGCTTCCAGATTAATTTCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTGTCATGATATTCAAGTTTCAGGAATGAGCCTTTGTAAT  
 ATAACCTGCTGTCAGCTCTGCTCTCTTTCCGTGAAGTTCAGCATGGGTGCTCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTGTCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTGAGAAATTTGCCCAACAT  
 AACTCAGTTCTGTGTGAGAGACAATTTAATAACAGTATAGATAATAATACCATATGATTTT  
 TTTAGTTGATGCTAAATGTAGATCCACCGTGGGAATCATTCCTTTAAATGACACGACA  
 GTCCACTCAAAGGATTGCCATAGCAATACAGCATCTTTTCTTTCTACTAGTCCAAGCCAAAA  
 TTTTAAGATGATTTGTGAGAAGGGCACAAAGTCTATCACTAATATTACAAGAGTTGGTA  
 AGCGCTCATCATTAATTTTATTTGTGGCAGGTATTATGACAGTGCAGCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCGGGTGGTTATGACCGCTACT  
 AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA  
 CAAAGGAATAATTTCTGATCCAGGATCGCTCTCAAATGGCTGATTTTATAAGGTTTGTG  
 AGCTGCACGTGAAGCATCTTATTTTATAGTATATCAACCTTTGTTTTTAAATGACCTGCCA  
 AGGTAGCTGAAGACCTTTTACAGAGTTCATCTTTTTTTTTTAAATTTTTTCTGCTCTTTAA  
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSS IIFAGGDKWSV DFRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPVRKVKV VVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQE HFGNYTCVAANKLGT TNASLPL  
NPPSTAQYGITGSADVL FSCWYLVLT LSSFTSIFYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

[illegible]

ATGAGTGTTCGATGGGAAGGATCTTTCTCCAAGTGTTCTCTTGTAGGGGAGCATTCTCTGCTGG  
 CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAGGAGGA  
 CGAGCTCTTGAGTGAGACCCAAACAGCTGCTTTTACCAAATTGCAATGGAGCCTTTTCAA  
 TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTTCAT  
 TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
 GCGGCTCCGGGTCTTGAGATGTAATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
 CCTTCTCCTTGCTGCAGTCAGCACACCTGGAGAACACTGGCTCAGGGTGATCAGAGGCTG  
 CAAGTCTCTCAGGCCCAACTCACCTGGGTCCGCGTCAAGCATGAGCACTTGTGTCAGCGGGT  
 AGACAACCTCACTCAGAACCCAGGGATGTTCAAGATCAAAGTGAAACAAGGCGCCCCAGGTC  
 TTCAAGGTCAACAGGGGGCCATGGGCATGCCTGGTGCCTTGGCCCGCCGGGACCACTGTCT  
 GAGAAGGGGAGCCAAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCTCGGAGCCCAAG  
 CCCACCGGGAGTCAAGGGAGAGGCGGGCTCTCAAAGGCCCAAGGTGCTCCAGGAGCAAG  
 GAGCCACTGGCACCACAGGACCCCAAGGAGAGAGAGGCGAGCAAGCGATGGGGGTCTCATT  
 GGCCCAAAAGGGGAACTTGAACCTAAGGGAGAGAGAAAGGAGCACTGGGTCTCCAGGAAGCAA  
 AGGGGACAGGGGATGAAAGGAGATGACAGGGTTCATGGGGCTCTTGGAGCCAGGGGAGTA  
 AAGGTGACTCTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTCTTGGAGCTAAAGGAGAT  
 CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCCTCTGGTGCAGTGGGACACCCAGGTGC  
 CAAGGGTGAGCCTGGCAGTGTGGCTCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGGA  
 GTCCAGGAGCCACAGGCTGAAAGGAAGCAAAGGGGACACAGGACTTCAGGACAGCAAGGA  
 AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCCAGG  
 GCTGGCAGGTCCAAGGGAGCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
 GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACTCAGTGTCC  
 GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
 GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGT  
 ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAAGATCTGGCTGGATAAT  
 GTTCAGTGTCCGGGACCGGAGAGTACCTCTGTGAGCTGCACCAAGATAGCTGGGGCCATCA  
 TGACTGTCCAGCAGGAGGAGCAGCGCTGGAGTGCAGCGCTCTGAGCCCCGAAACCCCTTTCA  
 CTCTCTGCTCTCCGAGGTGCTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
 TCCCTGGGGCAACTCAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA



## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPPAEKGAKGAMGRD  
GATGPGSGPQPPGVKGEAGLQGPQGAPGKQGATGTTPGPQGEKGSKGDGGLIGPKGETGTKEE  
KGDGLPGSKGDRGMKGADAGVMGPPGAQGSKGDGFRPGPPGLAGFPKAGKDGQGPGLQGVPG  
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSGATGLKGSKGDGTLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKDGQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW  
SCTKNSWGHHCDSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

00070103-10000000

**THE**

CCACGCGTCCGAAGGCAGACAAAGGTTCA TTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCAAACTCACCAGTGAGTGTGAGCATTTAAGAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAATGA GAAC TGATGGTACTTGTTTTAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCTCGAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAAC TGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCAAAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG  
TGATTCCTTGCAACAATCAATGA GAATCTTCATGTATTCTGGAGAACACCATTCTTGATTC  
CCCAACAATCAATCATAGTATAACTGTCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAGAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTAAACCAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAA

**SECRET**

&lt;subunit 1 of 1, 98 aa, 1 stop

MKLMVLVFTIGLTL LLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

**Important features:**

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

# FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCAGCCTGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCGGTGGTGGTGGAGGGG  
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCGCGCTCTGCTCGCGCCGAGATG  
 TGGAACTCTCCTTACAGAAACCGACTCTGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGTCTGGCGGGTGGCTTCTTCTCCTCGGCTTCTCTTCCGGTGGTTTA  
 TAAATCCTCCAATGAAGCTACTAACATTACTCCAAGGCATAATATGAAAGCATTTTTGGAT  
 GAAATTGAAAGCTGAGAAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
 AGGAACAGAAACAAAATTTTTCAGCTTGCAGCTTGCAGCAAAATTCATCCAGTGGAAGAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTTACCCAAATGAAGCTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCTC  
 AAGGAATGCCAGAGGCGATCTAGTGTATGTTAACTATGCACGAACCTGAAGACTTCTTTAAA  
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATGCGAGATATGGGAAAGT  
 TTTTCAGAGGAAATAAGGTTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT  
 CCGAGCTTGCTGACTACTTTTGTCTCTGGGGTGAAGTCTTATCCAGAGCGTTGGAATCTTCTCT  
 GGAGGCTGTGTCCAGCTGGGAAATATCTAAATCTGAATGGTCAGGAGACCTCTCCACACC  
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATGTCAGAGGCTGTTGGTCTTCCAA  
 GTATTCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCTAGAAAAAATGGGTGGC  
 TCAGCACCACCATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG  
 CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA  
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACACAGACAGATATGCTATT  
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATTTGTGAGGAGCTTTGGAACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGCAAATCTCTTATGAAAGTTGG  
 ACTAAAAAAGTCTTCCCCAGAGTTTCAAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG  
 AAATGATTTTGAAGTGTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCACGTTATATA  
 AAAATTTGGGAAACAAACAATTCAGCGCTATCCACTGTATCACAGTGTCTATGAACATAT  
 GAGTTGGTGGGAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG  
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTGATTGTGAGATTATG  
 CTGTAGTTTAAAGAAATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTTCAAGTGAAGACTCCAGGACTTTGACAAAAGCAACCAATAGTATTTAAGAA  
 TGATGAAATGATCAACTCATGTTTCTGGAAGAGCATTATTGATGCCATTAGGGTTACAGAC  
 AGGCTTTTATATAGGCATGCTATGCTCCAAGCAGCCACCAAGATGTCAGGGGAGTC  
 ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCTTCCAAGGCCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAAGTGCAGGACGCTGCAGAGACT  
 TTGAGTGAAGTAGCCTTAAGAGGATTTTATAGAGAATCCGTAATTTGAAATTTGTGGTATGTCA  
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTTGGTATATTTGAAATAAAGT  
 TGAATATTATATATA

## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARPRWLCAGALVLAGGFLLGFLGWFIKSSNEATNITPKHNMKAFI  
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDVSLAHYDVLLSYPNKTH  
PNYISIIINEDGNEIFNTSLFEPFPPPGYENVSDIVPFFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVIARYGKVFRGNKVKNQALAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQRGNILNLNGAGDPLTPGYPANERYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVVGPGFTGNFSTQVKVMMIHSTNEVTRIYNVIGTLRGAVEPDYV  
ILGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFLLGSTEW  
AEENSRLQERGVAYINADSSIEGNYTLRVDCITPLMYSLVHNLTKEKSPDEGFEGKSLYES  
WTKKSPSEFGMPRISKLGSNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSHVYET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHQ  
EMKTYSVSFDLSLFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHVIYAPSSHKNKYAGESFFGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE  
TLSEVA

### **Signal sequence:**

amino acids 1-40

### **N-glycosylation sites.**

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### **Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

### **N-myristoylation sites.**

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713